

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 18, 2004, 04:49:17 ; Search time 1365 Seconds  
(without alignments)  
5133.066 Million cell updates/sec

Title: US-10-020-095-4

Perfect score: 7348

Sequence: 1 MQGPPLTAHLLCVCTRAAL.....HSSVIFPCFKLLYFEMELWL 1428

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Xgapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QWTF=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNLIS=bits -START=1 -END=1 -MATRIX=biosum62  
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=2000000000 -USER=US10020095.@CGN\_1.1\_984 @runat\_10082004\_154042\_17445  
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:  
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4: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:  
5: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:  
6: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:  
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19: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3033	4535.50	Length: 880		

1	4535.5	61.7	3033	9	US-09-833-381-1810	Sequence 1810, Ap
2	3360	45.7	2273	16	US-10-108-260A-953	Sequence 953, App
3	2962.5	40.3	1880	13	US-10-112-944-160	Sequence 160, App
4	1819.5	24.8	1438	16	US-10-264-237-1040	Sequence 1040, App
5	1767.5	24.1	1459	13	US-10-276-774-601	Sequence 601, App
6	1542.5	21.0	6157	16	US-10-085-198-29	Sequence 29, Appl
7	1539.5	21.0	6069	16	US-10-085-198-27	Sequence 27, Appl
8	1529.5	20.8	6195	16	US-10-085-198-25	Sequence 25, Appl
9	1444.5	19.7	4492	13	US-10-096-625-199	Sequence 199, App
10	1441	19.6	4576	13	US-10-608-397-7	Sequence 7, Appl
11	1441	19.6	4576	15	US-10-292-081A-7	Sequence 7, Appl
12	1441	19.6	4577	14	US-10-052-817-1	Sequence 1, Appl
13	1441	19.6	4769	13	US-10-116-802-21	Sequence 21, Appl
14	1440	19.6	4422	9	US-09-873-403-4	Sequence 4, Appl
15	1440	19.6	4422	12	US-09-750-972-4	Sequence 4, Appl
16	1440	19.6	4577	9	US-09-873-403-3	Sequence 3, Appl
17	1440	19.6	4577	9	US-09-880-107-236	Sequence 236, Ap
18	1440	19.6	4577	10	US-09-960-706-654	Sequence 654, App
19	1440	19.6	4577	10	US-09-873-319-408	Sequence 408, App
20	1440	19.6	4577	12	US-09-750-972-3	Sequence 3, Appl
21	1440	19.6	4577	13	US-10-608-397-3	Sequence 3, Appl
22	1440	19.6	4577	13	US-10-608-397-5	Sequence 5, Appl
23	1440	19.6	4577	15	US-10-076-816-56	Sequence 56, Appl
24	1440	19.6	4577	15	US-10-292-081A-3	Sequence 3, Appl
25	1440	19.6	4577	15	US-10-292-081A-5	Sequence 5, Appl
26	1440	19.6	4577	16	US-10-331-496A-19	Sequence 19, Appl
27	1440	19.6	4577	16	US-10-159-563-136	Sequence 136, App
28	1440	19.6	4809	15	US-10-240-965-178	Sequence 178, App
29	1438	19.6	4527	10	US-09-756-247-3	Sequence 3, Appl
30	1438	19.6	4527	10	US-09-756-247-5	Sequence 5, Appl
31	1438	19.6	4527	17	US-10-312-309-3	Sequence 3, Appl
32	1438	19.6	4527	17	US-10-312-309-5	Sequence 5, Appl
33	1429	19.4	4530	13	US-10-608-397-2	Sequence 2, Appl
34	1429	19.4	4530	15	US-09-292-081A-2	Sequence 2, Appl
35	1422	19.4	4488	11	US-09-981-151A-9	Sequence 9, Appl
36	1422	19.4	4488	13	US-09-972-211-1	Sequence 1, Appl
37	1422	19.4	4488	13	US-10-096-625-1	Sequence 1, Appl
38	1418	19.3	4823	10	US-09-971-392-172	Sequence 172, App
39	1412.5	19.2	4595	9	US-09-917-800A-1531	Sequence 1531, Ap
40	1410	19.2	5092	10	US-09-971-429B-2	Sequence 2, Appl
41	1410	19.2	5092	15	US-10-006-285-404	Sequence 404, App
42	1400	19.1	4615	9	US-09-880-107-3727	Sequence 3727, Ap
43	1390	18.9	4615	15	US-10-006-285-405	Sequence 405, App
44	1384	18.8	4677	15	US-10-316-253-266	Sequence 266, App
45	1384	18.8	4701	15	US-10-316-253-268	Sequence 268, App

#### ALIGNMENTS

RESULT 1  
US-09-833-381-1810  
; Sequence 1810, Application US/09833381  
; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833.381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1810  
; LENGTH: 3033  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-833-381-1810

Alignment Scores:  
Pred. No.: 0  
Score: 4535.50  
Length: 880  
Matches:

Percent Similarity:	98.00%	Conservative:	2
Best Local Similarity:	97.78%	Mismatches:	1
Query Match:	61.72%	Indels:	17
DB:	9	Gaps:	1
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Db	6	GTCCGAAAATTCCTGTTTCAGCTTGTTTTAAAAATAAGATAAGCTATATTGGAGTAA	65
QY	566	ValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGlnProAspSer	585
Db	66	GTGAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACAGAGCTGACTCC	125
QY	586	IleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIle	605
Db	126	ATAGTITGGGATGTAGCTGTTGACAAAAGTGAATCTGATGAATGCCCTCTAATGATATT	185
QY	606	ThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGlyTyrTrpLeuGlyMet	625
Db	186	ACAAATGGAAAATGTGTCCTCAGCTTGGAACTTTATAACACAGGATATTATTTAGCGATG	245
QY	626	PheMetAsnSerPheAlaValPheGlnLysGlyLeuTrpValLeuThrAspAlaAsn	645
Db	246	TTTCATGAATTCITTTGCACTCTTTCAGGAATGTGGACTCTGGGTATTGACAGATGCAAC	305
QY	646	LeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMet	665
Db	306	CTCCAGAGGATTATTTGATGCTGTTTATGACAAATCGAAATATGCTCAGAGGTTTATG	365
QY	666	GluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGlySerSerProHis	685
Db	366	GAGGAAAATGAAGGACATATTGTAGATATTCAAGCTTTCTTTGGGTAGAGTCCACAT	425
QY	686	ValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsnMetGlyTyrArgIle	705
Db	426	GTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAATGGTTACAGGATT	485
QY	706	TyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPhe	725
Db	486	TACCAGGAATTTGAAGTAACTGTACCTGATTCTATCTACTTCTTGGGTGGCTACTGGTTT	545
QY	726	ValIleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPhe	745
Db	546	GTGATCTCTGAGGACCTGGGCTTTGGACTAACTACTCCAGTGAGGCTCCAAGCCTTC	605
QY	746	GlnProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAla	765
Db	606	CAACCATTTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGAGGTGAAGAATTTGCT	665
QY	766	LeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu	785
Db	666	TTGGAAATAACTATATTCCAAATTATTGAAAGATGCCACTGAGGTAAAGTAATCATTTG	725
QY	786	LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGln	805
Db	726	AAAAGTGACAAATTTGATTTCTAATGACTTCAATGAAATAAATGCCACAGCCACCAG	785
QY	806	GlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProThr	825
Db	786	CAGACCCCTTCTGGTTCCCGAGTGAAGTGGGCAACTGTTCTTTTCCCATCAGGCCACAC	845
QY	826	HisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSerAspAlaVal	845
Db	846	CATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTTCAACCACTGCTTCTGATGCTATC	905
QY	846	ThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeu	865
Db	906	ACCCAGATGATTTTAGTAAAGGCTGAAGGAATGAAAAATCATATTTCACATCCATCTTAA	965
QY	866	LeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhePro	885

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QY 1229 SerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAla 1248
Db 2106 TCCGCAAAATGGTTTGGATTGCTATTGTGCACCTCAATGTTGTAATAATGTGAAGGCT 2165
QY 1249 SerGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspVal 1268
Db 2166 TCTGGGCTCTTCTAGAGACGAAGATCTATCCAAAATCAAGAACCTTTGATTAGATGTT 2225
QY 1269 AlaValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPhe 1288
Db 2226 GCTGTAAAGAAATAAAGATGATCTCAATCATGTGGATTGATGTGTGTACAGCTTT 2285
QY 1289 SerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMet 1308
Db 2286 TCGGGCCCGGTAGGAGTGCATGCTCTTATGGAAGTTAAACCTATTAAGTGGCTTTATG 2345
QY 1309 ValProSerGluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly 1328
Db 2346 GTGCCCTCAGAACAATTTCTCTGACGGAGACAGTGAAGAAAGTGAATATGATCATGGA 2405
QY 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
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QY 1349 ValArgAsnPhelLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
Db 2466 GTGAGAAACCTTTAAAGTTTCAATATCCCAAGATGCTTCAGTGTCCATAGTGATTAATAT 2525
QY 1369 GluProArgArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAsp 1388
Db 2526 GAGCCAAAGAGACAGCGGTGAGAAAGTTACAACTCTGAAAGTGAAGCTGCTCTCTGTGAC 2585
QY 1389 LeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHis 1408
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QY 1409 HisSerSerValIlePheIlePheCysPheLysLeuLeuTyrPheMetGluLeuTrpLeu 1428
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RESULT 2
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; Sequence 953, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 953
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-953

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Score: 3360.00 Matches: 657
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.73% Indels: 0
DB: 16 Gaps: 0

US-10-020-095-4 (1-1428) x US-10-108-260A-953 (1-2273)

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QY 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60
Db 186 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCCACAGGTGACTGTGAAGCG 245
QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80
Db 246 GAGCTGCTCAGACAGCATCAAACTCACTGCTCTCTGCTCTGGAAGCAGAGAGAGTCTTT 305
QY 81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100
Db 306 GAAAAAGGCTCTTTTAAGACACTTACTCTCCATCACTACCTCTCAACAGTSCAGATGAG 365
QY 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120
Db 366 ATTATGAGCTACGTGTGTNACCGAGCTACCCAGGATGAGATTTTATTCTCTTAATAGTACC 425
QY 121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140
Db 426 CGCTATCATTTGAGACCAAGAGAAATATCTGCTCTTCAATCAACAGACAAGGCTTATAC 485
QY 141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160
Db 486 AAGCCAAAGCAAGAGTGAAGTTTCGCATTTGTACACTCTTCTCAGATTTTAAAGCCTTAC 545
QY 161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180
Db 546 AAAACCTCTTTAAACATCTCATTAAGGACCCCAANTCAATTTTGAATCCACACAGTGGTTG 605
QY 191 SerGlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIle 200
Db 606 TCACACAAAGTGAATCTTGGAGTCAATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 665
QY 201 LeuGlyAspTyrSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220
Db 666 CTTGGTGAAGTCTCTATTCAGTTCAAGTGAATGACGACATCACTATCATCAATTCAG 725
QY 221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240
Db 726 GTTTTCAGAAATATGATTATACCAAAATTTGAAGTGACTTTTCAGACACCATATATTGTTCT 785
QY 241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260
Db 786 ATGAATTTCTAAGCATTTAAATGGTACCACACGCAAGATATACATATGGGAAGCCAGTG 845
QY 261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTyrGlyLysLysLysAsnIle 280
Db 846 AAAGGAGACGTAAACGCTTACATTTTACCITTTATCCTTTTGGGGAAGAGAGAAAAATATT 905
QY 291 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300
Db 906 AAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAAATGATGAAGAGATGAAA 965
QY 301 AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320
Db 966 AATGTATGATTTCTTCAATGGACTTTCTGAATACCTGGAATCTATCTTCCCTGGACCA 1025
QY 321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340
Db 1026 GTAGAAATTTTAAACACAGTCACAGAAATCAGTTACAGGTATTTCAAGAAAATGTAAGCACT 1085
QY 341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 360
Db 1086 AATGTGTTCTTCAAGCAACATGATTACATCATGAGTTTTTTGATTATTACTACTGCTCTG 1145
QY 361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380
Db 1146 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACCTCGTGTGATGCAACCAACTG 1205
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; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 160
; LENGTH: 1880
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1867)
; US-10-112-944-160

1206 ACTCTTGAAGAAAGAAATAATATGATCATACAGTGCACAGAGAACTATCTGAG 1265
401 TTTTTPSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420
1266 TACTGGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAGAAATAAATAT 1325
421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerGlu 440
1326 ACTGTCCCCAAGTGGAACTTTTAAGATTGAATCCCAATCTCGAGGATCCAGTGGAG 1385
441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSerLeuPhe 460
1386 CTACAGTTGAAGCCCTATTTCTTGGTAGTAAAGTAGCATGGCAGTTTCATGCTGTTT 1445
461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480
1446 AAGTCTCTTAGTAAGACATACATCCAACTAAACAAAGAGATGAAATAATAAGGTGGGA 1505
481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500
1506 TCSCCTTTTGGATTGGTGGTAGTGGCAACAACGATTGAAGGATTAGCTATATGGTA 1565
501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520
1566 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAACAAATAATCAACAATGTTCTTTTAA 1625
521 ProGluAsnSerThrProLysAlaCysValIleValTyrIleGluAspAspGly 540
1626 CCAGAAATTTCTTGGACTCCAAAGGCTGTGAATTTGTATTATATTGAAGATGATGG 1685
541 GluIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560
1686 GAAATTAATAGTGATGTTCTAANAATCTGTTCAGCTGTTTAAATAAGATAAAG 1745
561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580
1746 CTATATTGGAGTAAAGTGAAGCTGAACCATCTCGAGAAAGTCTCTCTTAGGATCTCT 1805
581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600
1806 ACACAGCTGACCTCATAGTTGGATTGAGTTGACCAAAAGTGTGATCTGATGAT 1865
601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620
1866 GCCTCTAATGATATTACAATGGAATATGTGTCATGAGTTGGAACCTTTATAACAGGA 1925
621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTyrVal 640
1926 TATTATTAGCGATGTTTCATGAATCTTTTTCAGTCTTTCAGGAAATGTGAGCTCTGG 1985
641 LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsn 657
1986 TTGACACATGCAACCTTCAGAGGATTATATTGATGGTGTGTTTATGACAAAT 2036

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## RESULT 3

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US-10-112-944-160
; Sequence 160, Application 'US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrul
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and

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; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 160
; LENGTH: 1880
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1867)
; US-10-112-944-160

Alignment Scores:
Pred. No.: 3,43e-288 Length: 1880
Score: 2962.50 Matches: 587
Percent Similarity: 96.23% Conservative: 0
Best Local Similarity: 96.23% Mismatches: 2
Query Match: 40.32% Indels: 21
DB: 13 Gaps: 1

US-10-020-095-4 (1-1428) x US-10-112-944-160 (1-1880)

QY 1 MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu 20
DB 80 ATGAGGGCCACCGCTCTCTGACCGCCGCCACCTCTCTGGGTGTCACCGCGGCTG 139
QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleAsnProGlyGly 40
DB 140 GCCGTGGCTCCCGGCTCTGGTTCGTGTGACAGCCCGGCGATCATCAGGCCCGGAGGA 199
QY 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60
DB 200 AATGTGACTAATGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGCG 259
QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80
DB 260 GAGCTGCTCAAGACAGCATCAAACTCACTCTCTCTCTGGAAGCAGAGGAGTCTTT 319
QY 81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100
DB 320 GAAAAAGCTCTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 379
QY 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120
DB 380 ATTTATGAGCTACGTGTAAACCGGACGTACCCAGGATGAGATTTTATTTCTCTAATAGTACC 439
QY 121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140
DB 440 CGCTTATCATTTGAGACCAAGAGATATCTGTCTTCATTCAACAGACAGAGCCCTTATAC 499
QY 141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160
DB 500 AAGCAAAAGCAAGAGTGAAGTTTCGATGTTTACACTCTTCTCAGATTTTAAAGCCCTTAC 559

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Db 302 CAAGAAGAAATAGCTTGGTGGTGTGGTCTACTCAGGATACCACTGGCTTTAAAGGCT 361  
 Qy 1191 LeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThr 1210  
 Db 362 CTGTCTGAATTCAGCCCTTAATGAATACAGAAGGACAAATATCCAAGTGACCGTGACG 421  
 Qy 1211 GlyProSerSerProSerPro----- 1217  
 Db 422 GGGCTAGCTACCAAGTCTCTGTAAGTTCCTGATTGACACACACACACCGCTTACTCCCT 481  
 Qy 1218 -----LeuAlaValValGlnProMetAlaValAsnIleSerAlaAsnGlyPhe 1233  
 Db 482 CAGACAGCAGAGCTGTGTGGTACAGCCAAATGGCAGTTAATATTTCCGCAATGGTTTT 541  
 Qy 1234 GlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArg 1253  
 Db 542 GGATTCCTATTTGTGAGCTCAATGTTGTATATATATGTGNAAGCTTCTGGTCTTCTAGA 601  
 Qy 1254 ArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsn 1273  
 Db 602 AGACGAAGATCTATCCAAATCAAGAGCCTTTCAATTTAGATCTTGTCTGTAAAGAAAAAT 661  
 Qy 1274 LysAspSerLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyProGlyArg 1293  
 Db 662 AAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAGCTTTTCGGGCCCGGTAGG 721  
 Qy 1294 SerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSerGluAla 1313  
 Db 722 AGTGGCATGGCTCTTATGGAAGTTAACTATTAAAGTGGCTTTATGGTGGCTTCAGAAGCA 781  
 Qy 1314 IleSerLeuSerGluThrValLysLysValGluTyrAspHisGlyLysLeuAsnLeuTyr 1333  
 Db 782 ATTTCTCTGAGCAGACAGTGAAGAAAGTGGAAATATGATCATGGAAGAACTCAACCTCTAT 841  
 Qy 1334 LeuAspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLys 1353  
 Db 842 TTAGATTCTGTAAATGAACCCAGTTTGTGTTAATATCTCTGCTGAGAACTTTAAA 901  
 Qy 1354 ValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGln 1373  
 Db 902 GTTTCAAATACCCAAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCAAGACAG 961  
 Qy 1374 AlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspVal 1393  
 Db 962 CGGTGGAAGAGTTACAACTCTGAAGTGAAGCTGTCTCTGAGCTTTGCGAGTGATGTC 1021  
 Qy 1394 GlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHisSerSerValIle 1413  
 Db 1022 CAGGGCTGCCGTCTCTGTGAGGATGGAGCTTCAGGCTCCCATCATCTTTCAGTCAAT 1081  
 Qy 1414 PheIlePheCysPheLysLeuLeuTyrPheMetGluLeuTrpLeu 1428  
 Db 1082 TTTATTTCTGTTTCAAGCTCTGTACTTTATGGAACCTTTGGCTG 1126

RESULT 5

US-10-276-774-601/c  
 ; Sequence 601, Application US/10276774  
 ; Publication No. US20040053245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: US/10/276,774  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 09/496,914  
 ; PRIOR FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO 601  
 ; LENGTH: 1459

; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-276-774-601  
 Alignment Scores:  
 Pred. No.: 9,72e-168 Length: 1459  
 Score: 1767.50 Matches: 359  
 Percent Similarity: 94.01% Conservative: 2  
 Best Local Similarity: 93.49% Mismatches: 1  
 Query Match: 24.05% Indels: 22  
 Gaps: 1  
 US-10-020-095-4 (1-1428) x US-10-276-774-601 (1-1459)  
 Qy 1067 AspValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsn 1086  
 Db 1455 GAGGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAGAGGAATTCAGACAAT 1396  
 Qy 1087 TyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGlu 1106  
 Db 1395 TATACTCTAGCCCTATAAATATGATTCATCAGTGGGAGTCTCTAAAGCGAAGAA 1336  
 Qy 1107 AlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrpValSer 1126  
 Db 1335 GCTTTGAATATGCTGACTTGGAGAGCAGAACAGAGGTGGCATGCAATTCGGGTGTCA 1276  
 Qy 1127 SerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAla 1146  
 Db 1275 TCAGAGTCCAAACTTCTGACTCTCTGGCAGCAGCCCTCCCTGGATATTGAAGTTGCAGCC 1216  
 Qy 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArg 1166  
 Db 1215 TATGCACTGCTCTCACACTTCTTCAATTTTCAGACTTCTGAGGGAATCCCAATTTATCAGG 1156  
 Qy 1167 TrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrVal 1186  
 Db 1155 TGGCTAGCAGCGCAAGAAATAGCTTGGTGGTGTTCATCTACTCAGGATACCACTGTG 1096  
 Qy 1187 AlaLeuLysAlaLeuSerGluPheAlaLeuMetAsnThrGluArgThrAsnIleGln 1206  
 Db 1095 GCTTTAAAGGCTCTGTCTGAAATTTGCAGCCCTAATGAATACAGAAAGACAAATATCCAA 1036  
 Qy 1207 ValThrValThrGlyProSerSerProSerPro----- 1217  
 Db 1035 GTGACCGTGTACGGGCGCTAGCTCACCAGTCTCTGTAAGTTCCTGATTGACACACAAAC 976  
 Qy 1218 -----LeuAla-ValValGlnProMetAlaVal-AsnIle 1229  
 Db 975 CGCTTACTCTTCAGACAGCAGCTTGTGATGGTACAGCAATGGCAGTGTAATATTT 916  
 Qy 1229 erAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAla 1249  
 Db 915 CCGCAATAGTTTGGATTTGCTATTTGTCACTCAATGTTGTATATAATGTGAAGCTT 856  
 Qy 1249 erGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspVal 1259  
 Db 855 CTGGGTCTCTAGAGAGCAGAGATCTATCCAAATCAAGAGCGCTTTGATTAGATGTG 796  
 Qy 1269 laValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPhe 1289  
 Db 795 CTGTAAAGAAATTAAGATGATCTCAATCATGTGGATTGGAATGTGTGTACAGCTTTT 736  
 Qy 1289 erGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMet 1309  
 Db 735 CGGGCCCGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTATTAAAGTGGCTTTATGG 676  
 Qy 1309 alProSerGluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly 1329  
 Db 675 TGCCCTTCAGAGCAATTTCTCTGAGCGGAGACAGTGAAGAAAGTGAATATGATCATCGAA 616  
 Qy 1329 ysLeuAsnLeuTyrLeuAspSerValAsnGlnThrGlnPheCysValAsnIleProAla 1349  
 Db 615 AACTCAACCTCTATTAGATTCTGTAATGAACCCAGTTTGTGTTAATATATCTCTGCTG 556

QY 1349 alArgAsnPhelysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTrpG 1369  
 Db 555 TGAGAACTTTAAAGTTTCAAAATACCAAGATCTTCAGTGTCATAGTGGATTACTATG 496  
 QY 1369 luProArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAspL 1389  
 Db 495 AGCAAGGAGACAGCGGCGTGAAGATTACAACTCTGAAGTGAAGCTGTCTCTGTGACC 436  
 QY 1389 euCysSerAspValGln-GlyCysArgProCysGluAspGlyAlaSerGlySerHisHis 1408  
 Db 435 TTTGCAGTGATGTCAGAGCTGCCGCTCTTGTGAGGATGGAGCTTCAGGCTCCCATCAT 376  
 QY 1409 HisSerSer-ValIlePhePheCysPheLysLeuLeuTyrPheMetGluLeuTrpL 1428  
 Db 375 CACTCTTCGAGTCGATTTTATTCTTCTGTTTCAAGCTTCTGTACTTTATGGAACITTTGGC 316  
 QY 1428 eu 1428  
 Db 315 TG 314

## RESULT 6

US-10-085-198-29  
 ; Sequence 29, Application US/10085198  
 ; Publication No. US2004000907A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alcobrook et al.  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-279  
 ; CURRENT APPLICATION NUMBER: US/10/085,198  
 ; PRIORITY FILING DATE: 2002-02-25  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR FILING DATE: 2001-08-13  
 ; PRIOR FILING DATE: 2001-08-13  
 ; PRIOR FILING DATE: 2001-08-16  
 ; PRIOR FILING DATE: 2001-08-16  
 ; PRIOR FILING DATE: 2001-02-27  
 ; PRIOR FILING DATE: 2001-03-20  
 ; PRIOR FILING DATE: 2001-03-20  
 ; PRIOR FILING DATE: 2001-04-21  
 ; PRIOR FILING DATE: 2001-06-20  
 ; PRIOR FILING DATE: 2001-08-29  
 ; PRIOR FILING DATE: 2001-02-28  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 653  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 29  
 ; LENGTH: 6157  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-085-198-29

Alignment Scores:  
 Pred. No.: 5,76e-144 Length: 6157  
 Score: 1542.50 Matches: 494  
 Percent Similarity: 41.65% Conservative: 257  
 Best Local Similarity: 27.40% Mismatches: 555  
 Query Match: 20.99% Indels: 497  
 DB: 16 Gaps: 57

US-10-020-095-4 (1-1428) x US-10-085-198-29 (1-6157)

QY 5 ProLeuLeuThrAlaAlaHisLeuLeuCysValCys-----ThrAlaAlaLeu 20  
 Db 360 CCGTTGCTCCGCTCTCTGCTCTCTGCTGTCGCGCGGAGCGGCTGCGCGGCGAG 419

QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40  
 Db 420 CCTCAGGCCCGCGGT-----TACTTGATTCAGCTCCCTCTGTTTTCGCGCGGCGTG 473  
 QY 41 AsnValThrIleGlyValGluLeuGluHisCysProSerGlnValThrValLysAla 60  
 Db 474 GAGGAAGTCATCAGCGTGCACATCTTT---AACTCTCAAGGGAAGTCCAGCTCCAGCT 530  
 QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGly---Val 79  
 Db 531 CAGCTGGTGGCCCGGCTGAG-----CGGTGGTGCAGAGCCAGGAGGCCCATC 578  
 QY 80 PheGluLysGlySerPhePheLeuThrLeuProSerLeuProLeuAsnSerAlaAsp 99  
 Db 579 CTGATAAAGGACAAATCAAA---CTCAAGGTGCCACCGGCTCCCGGGGCAAGCG--- 632  
 QY 100 GluIleTyrGluLeuArgValThrGlyArg-----ThrGlnAspGluIlePhe 116  
 Db 633 -----CTTCTGAAAGTGTGGGCGCGGCTGGAGCGGAGGAGGGCCCTCTTT 683  
 QY 117 SerAsnSerThrArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAsp 136  
 Db 684 CACAACACAGACCTCGGTGACCGTGCAGCGCGGCGGCTTCTGTATTTCATCCAGACGAC 743  
 QY 137 LysAlaLeuTyrLysProLysGlnGluValLysPheArgIleValThrLeuPheSerAsp 156  
 Db 744 AAGCTGTGTACAGACCCAGCAGCAGTGTCTATAAGCATCTTCACGCTCTCTCCAAT 803  
 QY 157 PheLysProTyrLysThrSerLeuAsnIleLeuLysAspProLysSerAsnLeuIle 176  
 Db 804 CTGAGGCTGTCAACGAGAACTGGAAGCTACATCTCTGGACCCCGGAGGCTCTCGGATG 863  
 QY 177 GlnGlnTrpLeuSer---GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeu 195  
 Db 864 ATAGAGTGGAGACACTTAAAGCCGTTCTGTCTGCGGCATCAACAACATGAGCTTCCCTTG 923  
 QY 196 SerSerHisProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThr 215  
 Db 924 TCCGACAGCCTGTGTGGAGAAATGTTCAATTTTGTGAATGCAAGGCCAGCGGTAC 983  
 QY 216 TyrGlnSerPheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThr 235  
 Db 984 AACAAAGTCTTTGAAGTTTCAGAAGTATGTGTGTCCTTGAAGTTTGAAGTTTGAAGTT 1043  
 QY 236 ProLeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThr 255  
 Db 1044 CCGCGGTATATCCAAAGACCTGGACGCTGTGAGACAGGCACTGTGCGGCGCAGGTATACC 1103  
 QY 256 TyrGlyLysProValLysGlyAspValThr-----LeuThrPheLeuProLeuSerPhe 273  
 Db 1104 TTTGGAAACCTGTGGCTGTGCTTAACGATCAACATGACTGTTAATGTTAGGTAGGTAC 1163  
 QY 274 TrpGlyLysLys-----LysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsn 291  
 Db 1164 TACAGCCACGAGTGGGAGCGGCTGTCTCAGAAACAACCAAGATCTCTCGGCTCCAGGAC 1223  
 QY 292 PheSerPheAsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGlu 311  
 Db 1224 TTCACATCTCGGTAGGACATG-----GlyProValGluIleLeuThrThrVal 1247  
 QY 312 TyrLeuAspLeuSerSerPro-----GlyProValGluIleLeuThrThrVal 327  
 Db 1248 ---ATCCCGAGCGGACGTCCTCGACACTTCGCGGCGGAGGTCAGCATCTCTGGGCCATGGTG 1304  
 QY 328 ThrGluSerValThrGlyLysLeuArgAsnValSerThrAsnValPhePheLysGlnHis 347  
 Db 1305 ACC---AGTGTGACGCGGAGCCAGCAG----- 1328  
 QY 348 AspTyrIleIleGluPhePheAspTyrThrThrVal----- 359  
 Db 1329 -----GTCCGGTTTCGATGACTTCCACCCCGCTGCGAGAGGAGCTGGTGCATCCGG 1379

Qy 360 -----LeuLeuProSerLeuAsnPheThrAlaThrValIys 371  
 Db 1380 TACTCCAAGACACGAGGAGCAATTCAAGCCGGGCTGCTACCTACCTGGGAGAGTGGAG 1439  
 Qy 372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsnValValIle 391  
 Db 1440 CTATCTACCCCGATGCGAGCCCA-----GCTCAGGGGTGACGGTC 1481  
 Qy 392 ThrValThrGlnArgAsnThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnIys 411  
 Db 1482 CAGATT-----AAG 1490  
 Qy 412 MetGluAlaValGlnIysIleAsn-----TyrThr-----ValProGlnSerGlyThr 427  
 Db 1491 GCGAGCTGACACCAAGGATAATCTACACAGTGGAAGTGTGTCCAGCGTGACTA 1550  
 Qy 428 PheLysIleGluPheProIleLeuGluAspSerSerGlu-----LeuGlnLeuLys 444  
 Db 1551 GTGGGGTTTGAATCCCTCCATCCCACTGAGCCAGCGTGTGGTGGAGACCAAG 1610  
 Qy 445 AlaTyrPheLeuGlySerLys-----SerSerMetAlaVal 456  
 Db 1611 GTATGCGACTGAACCGGAAGCCGCGGGGGCTCAGTACTGCCCGAGCTACCTCTCCCTC 1670  
 Qy 457 HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsn 476  
 Db 1671 GGCAGCTGGTAC---TCCCCAGCCAGTACTACTGAGTGCAGCCAGCCACCTCCACCCA 1727  
 Qy 477 IleLysValGlySerProPheGluLeuValValSerGlyAsnLysArgLeuLys---Glu 495  
 Db 1728 CTGCAGGTTGGGAAGAAGCTATTTCTGTGAAGTCCCATGTCCCTCGCACTTTACC 1787  
 Qy 496 LeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLysGln----- 512  
 Db 1788 CTGTACTACAGGTGGCTGCACGGGCAATATGTCTATCGGCCAGCAGCGCTGCCAC 1847  
 Qy 512 ----- 512  
 Db 1848 ACCACCAGCAGCGAAGCGGGGGCCCTGCTCGAGAAACCGATTGTTTAAACA 1907  
 Qy 513 -----Asn 513  
 Db 1908 CACCTTCTGAGACAGAGCCCCACAGCCCGAGAGCTGAGTGCAGCTGTGTGAC 1967  
 Qy 514 SerThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleVal 533  
 Db 1968 TCTCTTCATCTGCGCGTGACCCCG-----AGCATGGTCCCTTGGTCCCTGTGTGTC 2021  
 Qy 534 TyrTyrIleGluAspGlyGluIleIleSerAspValLeuLysIleProValGlnLeu 553  
 Db 2022 TTCTACCTCAGGAGATGAGAGGGGCTCCGACAGACCTTCAGTTTCAGTCGAGACC 2081  
 Qy 554 ValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLys 573  
 Db 2082 TTCTTGGAAACACAGTTTCAGTACGTATTACAAATGACACCAACCTGGGGAGGTT 2141  
 Qy 574 ValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaValAsp 593  
 Db 2142 GTGCACCTGCGGATCAGGGTGTGAAGG---GGCAGCTGTGTGCGCTGCGCGAGTTGAT 2198  
 Qy 594 LysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValValHsGlu 613  
 Db 2199 AAGAGTGTCTACCTGTCTCAGGTCTGGGTTCGGCTGACTCTCCCTCCAGGTTTTCAGGAA 2258  
 Qy 614 LeuGluLeuTyrAsnThrGly----- 620  
 Db 2259 CTGGAAGATTATGATGTTTCTGATTCTCTTGGGTGTGTCCAGGAGGATGTCCTTTTGG 2318  
 Qy 621 -----TyrTyrLeuGly 624  
 Db 2319 TGGGCTGGGTGAGCGCACACGACCGCGGGCTCTCTGTCTTCCCGTGGCCCTGGGGC 2378  
 Qy 625 MetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAsp--- 643

Db 2379 ATCCACAGGACTCTGGTTTGCCTTCACGAAACGGGACTGGTGTGATGACCGACCGA 2438  
 Qy 644 AlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyrAlaGluArg 663  
 Db 2439 GTGAGCTGAACACACCGCAGGACGCTGGCTCTAC-----ACCGATGAGGCTGCTCCC 2492  
 Qy 664 PheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGlySerSer 683  
 Db 2493 GCTTTCAGCCCCACACAGGAGCCTGTG-----GCGTGGCTCTCTTC 2537  
 Qy 684 ProHis-----ValArgLysHisPheProGluThrTrpIleTrp 696  
 Db 2538 AGGCACCCCCCGACAGAGAGAGAGAAAGGACTTCTTCCCGAAGATGATGTTGG 2597  
 Qy 697 LeuAspThrAsnMetGlyTyrArgIleTyrGln---GluPheGluValThrValProAsp 715  
 Db 2598 CATTGTCTCAACATCAGTACCCCATCTGGTGAAGGACACTCAGTGTGAAGTCCCGGAC 2657  
 Qy 716 SerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeu 735  
 Db 2658 TCCATCACCAGCTGGTGGGTGAGCGCTGCTCCACCTCTCAGGCTTAGGCATC 2717  
 Qy 736 ThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuPro 755  
 Db 2718 ---GCCGAGCCCTCCCTGCTGAAGACCTTCAAGCCCTTCTCGTGGACTTCATGCTCCCC 2774  
 Qy 756 TyrSerValIleArgGlyGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLys 775  
 Db 2775 GCTCTCATCTCCGTGGGAGCAGTCAAGATCCGCTCAGTGTCTACACTACATGGGC 2834  
 Qy 776 AspAlaThrGluVal-----LysValIleIleGluLysSerAspLysPheAspIleLeu 793  
 Db 2835 ACCTGCGCTGAGGTGTACATGAAGCTCTCGGTCTCCCAAGGGCATCCAGTTT--- 2885  
 Qy 794 MetThrSerSerGluIleAsnAlaThrGlyHis-----GlnGlnThr 807  
 Db 2886 -----GTTGGGATCTCTGGCAACGCCATGTGACCAAGAAG 2921  
 Qy 808 LeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProHisLeu 827  
 Db 2922 ATGTGTGTGGCCCGGAGGCTGAGCCCATCTGGGTCTGTCTCTCTCTCCTTCAGCGACTG 2981  
 Qy 828 GlyGluIleProIleThrValThrAlaLeuSer----- 838  
 Db 2982 GGACTCAACACATCAGCGCCAAAGCCCTTGTCTACGAGACACAAATTCCTGCGCGGAT 3041  
 Qy 839 -----ProThrAlaSer 842  
 Db 3042 GGGAGTCCAGCAACACCCCTGAGGAGAAATCACGCCGACAGGAGGTCCTCCATCGGGGTG 3101  
 Qy 843 AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln 862  
 Db 3102 GATCAGCTCAGCGCAGTGTGATGTTGAGCGGAGGAGTCCCGCGGCTACACCTAC 3161  
 Qy 863 SerIleLeu----- 865  
 Db 3162 AGCGCATTTCTGTCTCCAGTGAGAGAGTCCACATCTCCACCCCAACAAGTATGAGTTC 3221  
 Qy 866 -----LeuAspLeuThr----- 869  
 Db 3222 CAGTATGTGACGCGCCACTGCGCTCACCCGCTTGTGTGTGGTGTGTGCGAGCTCACAAT 3281  
 Qy 870 AspAsnArgLeu----- 873  
 Db 3282 GATCGCGGTGGCTTGTCTTCTGGGCCCCCAGGACACAGGAGCATGATCGAGATCGTC 3341  
 Qy 873 ----- 873  
 Db 3342 CTGGGGGGCATCAGAACACCAGGTTCATGGATCTCCACAGCAAGATGGGAGAGCCCGTG 3401  
 Qy 874 -----GlnSerThrLeuLysThrLeuSerPhe----- 882

Db 3402 GCAGTGCACACACGCGCAAGATCTCTCTCGGATCAATTCAGAACATTCGTGATCAGC 3461  
QY 882 ----- 882  
Db 3462 TGGCGTGGTGGCCCTTATCCAGGTTGGCCATGGTCCAGAGCCATCCAAATGAGTCTGTCTC 3521  
QY 882 ----- 882  
Db 3522 GTGGCCTGGACCTCCCGAGGCCACAGAGGTCACAGTTCATTGGCTTTTCCACCGGCTGG 3581  
QY 882 ----- 882  
Db 3582 GGCTCCATGGGTGAATTCGAATCTGGAGAGATGGAGGTGACGAGGTACAGCGAG 3641  
QY 883 -----SerPheProProAsnThrValThrGlySerGluArgValGlnIleThr 898  
Db 3642 GCCTTCACCTCGGGTCCACACGCGCATCCCTGGGTCTGAGCGACCCGCGCTCC 3701  
QY 899 AlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetPro 918  
Db 3702 ATCATCGGGAGCTCATGGGGCCCAACCCCTGAACACCTCAACACACCTCTCGGCTGGCG 3761  
QY 919 TyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyr 938  
Db 3762 TTTGGCTGTGGAGAGCAGACATGATCCACTTTGCCACCCAAAGCTTTGTCTGAGTAT 3821  
QY 939 LeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLeuAlaLeuSerPheMetArg 958  
Db 3822 CTTCAAGAAACCCAGCAGCTCAGCCCTGAGGTGGAGAGAGACACCCAGCTACCTAGTA 3881  
QY 959 GlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGly 978  
Db 3882 CAAGGCTACCGAGCGCCAGCTGACCTCAAGCGCCAGAGTGGCTTACAGCGCTTTGGG 3941  
QY 979 AsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGlu 998  
Db 3942 GAGCGGACGATCGGGAGCATGTGGCTCACAGCCTTTGTCTGAAGCTTTCGCACAG 4001  
QY 999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLys 1018  
Db 4002 GCTCGCAGCTTTATCTCTGGACCCCGGAGCTGGCTCGCCGAGAGCTGGATCATC 4061  
QY 1019 GlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeu 1038  
Db 4062 CAGCAGCAGCAGCCGATGCTCTCTCTGGCGCTGGCAGGCTCTGACAAAGACATC 4121  
QY 1039 GlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeu--- 1057  
Db 4122 CAGGTTGGATCCACGCGATTTGCTCCGCTGACAGCCTACGCTGCTGCTCTCTGGAA 4181  
QY 1058 ---GlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGlu 1076  
Db 4182 ACAGGCACAGCCTCAGAGGAGGAGAGGCTCCACTGACAAAGCGAGGACATCTCTGGAG 4241  
QY 1077 SerGluPheSerArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeu 1096  
Db 4242 TCTGCTGGCCCTCGGCCATG---GACCTTATAGCTGTGCCCTGACTACCTACGCGCTG 4298  
QY 1097 SerSerValGlySerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGlu 1116  
Db 4299 ACCCTGCTCGGACCGCGAGCCCTGAGGCACTCGCAAGCTCGTACGCTGGCCATC 4358  
QY 1117 GlnGluGlyMetGlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGln 1136  
Db 4359 ATCGGAGATGGGTCAACCCACTG-----AGCTGTCAAAATCTCTGGGAC 4403  
QY 1137 ProArg-----SerLeu 1140  
Db 4404 GTGCAAAAGGCGACATCTTGAGCTTCAGTACAGGGTCTCTCAGTCAAGTGTCTCGGC 4463  
QY 1141 AspIleGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu 1160  
Db 4464 GTGAGAAATGACACCTACGCGCTTCTGACCTACACTCTGCTGGGTGACGTGGCTGCC 4523

## RESULT 7

US-10-085-198-27  
; Sequence 27, Application US/10085198  
; Publication No. US20040009907A1

QY 1161 GlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyIlePheAlaSer 1180  
Db 4524 GCCCTGCTGTGGTGAAGTGGCTGTCCAGCAGCGAAATGCACTTGGGGTCTTCTCTCC 4583  
QY 1181 ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaLeu----- 1197  
Db 4584 ACTCAGGACACCTGGTGGTCTTCAGGCGCTTGGCTGAATATGCAATCTTCTCTATGCT 4643  
QY 1198 -----Met 1198  
Db 4644 GGAGCATCACTCAGTCTCTCCCTGGCCTCCACCACTGGACTACCAGAAACCTTC 4703  
QY 1199 AsnThrGluArgThrAsnIleGlnValThrValThrGly-----ProSerSerProSer 1216  
Db 4704 GAGCTGCACAGGACCAACAGAGAGTTCTGCAGACAGCAGCGATCCCCAGCTCCCCACG 4763  
QY 1217 ProLeuAlaValValGlnProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAla 1236  
Db 4764 GGGCTGTTTGTG-----AGTGCCAAAGGGGAGCGGTGTGTGC 4799  
QY 1237 IleCysGlnLeuAsnValValTyrAsnValLys-----AlaSerGlySerSerArg 1253  
Db 4800 CTGATGCAGATGTATGTACCTCAATGTGCTGACCGGTGGCCAAAGCCAGCTTTCAG 4859  
QY 1254 ArgArgArgSerIleGlnAsnGlnGlu----- 1262  
Db 4860 CTGCTCGTAAGCCTCCAGGAGCCTGAGGCCCGCAGGAGCGCCCGCCCTGCTGCTGCT 4919  
QY 1263 -----AlaPheAspLeuAspValAlaValLys 1271  
Db 4920 GCAGCTGAGGTTCCCGAGGAGACTGGCCCCCAGCTGACGATGATGACCCAGCGCCGAT 4979  
QY 1272 GluAsnLysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyPro 1291  
Db 4980 CAGCATCACAGGAATACAAG---GTGATGCTGGAGGTGTGCACACAGTGTGCTCATGCA 5036  
QY 1292 GlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311  
Db 5037 GGTCTTCCAATATGCTGTCTCTGGAGTGGCCCTGCTGTGCTGCTGCTGCTGCTGCTGCT 5096  
QY 1312 GluAlaIleSerLeuSerGluThr-----ValLysLysValGlu 1324  
Db 5097 GAG-----AGCCTGGAGCAGCTGTCTCTTGCACAGCAGCATGGGGATGAGAGGTATGAA 5150  
QY 1325 TyrAspHisGlyLysLeuAsnLeuTyrLeuAspSerVal---AsnGluThrGlnPheCys 1343  
Db 5151 GTGGCTGACGCCGAGTGTCTTCTACTTTGATGAGATCCCGCCCGGTGCTGCTGCTGCTGCT 5210  
QY 1344 ValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSer 1363  
Db 5211 GTGGGTTCCGTGCTCTCCGGAGTGGCTGTGGCGAGGAGCTGGCGCTGCCAGTCTCC 5270  
QY 1364 IleValAspTyrTyrGluProArgGlnAlaValArgSerTyrAsnSerGluVal--- 1382  
Db 5271 GTGTACGACTACTACGAACCGCTTCGAGGCCACTCGCTTCTACAAAGCTCAGCAGCGAC 5330  
QY 1383 -----LysLeuSerSerCysAspLeuCysSerAspValGln----- 1394  
Db 5331 AGCCCACTGGCCGGGAAGTGTGGCGGACCCCGGTGCAACGAAGTGGAGCGGCCCT 5390  
QY 1395 -----GlyCysArgProCysGluAspGlyAlaSerGlySerHisHisSer 1410  
Db 5391 GCCCGGGCGCGGCTGTCTCCCGGAGTCCGGCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 5450  
QY 1411 SerValIle 1413  
Db 5451 GCGGCGATC 5459

## GENERAL INFORMATION:

APPLICANT: Alsbrook et al.  
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 FILE REFERENCE: 21402-279  
 CURRENT APPLICATION NUMBER: US/10/085,198  
 CURRENT FILING DATE: 2002-02-25  
 PRIOR APPLICATION NUMBER: 60/271,646  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/276,401  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/311,981  
 PRIOR FILING DATE: 2001-08-13  
 PRIOR APPLICATION NUMBER: 60/312,858  
 PRIOR FILING DATE: 2001-08-16  
 PRIOR APPLICATION NUMBER: 60/271,840  
 PRIOR FILING DATE: 2001-02-27  
 PRIOR APPLICATION NUMBER: 60/277,324  
 PRIOR FILING DATE: 2001-03-20  
 PRIOR APPLICATION NUMBER: 60/286,096  
 PRIOR FILING DATE: 2001-04-21  
 PRIOR APPLICATION NUMBER: 60/299,695  
 PRIOR FILING DATE: 2001-06-20  
 PRIOR APPLICATION NUMBER: 60/315,614  
 PRIOR FILING DATE: 2001-08-29  
 PRIOR APPLICATION NUMBER: 60/272,405  
 PRIOR FILING DATE: 2001-02-28  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 653  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 27  
 LENGTH: 6069  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-085-198-27

## Alignment Scores:

Pred. No.: 1,13e-143 Length: 6069  
 Score: 1539.50 Matches: 493  
 Percent Similarity: 41.60% Conservative: 257  
 Best Local Similarity: 27.34% Mismatches: 556  
 Query Match: 20.95% Indels: 497  
 DB: 16 Gaps: 57

US-10-020-095-4 (1-1428) x US-10-085-198-27 (1-6069)

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DB	406	AAGCTGTGTACAGACCCACGACCGAGTGTCTATAAGCACTTCACCGTCTCCCAAT	465
QY	157	PhelysProTyrLysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIle	176
DB	466	CTGAGGCTGTCAACGAGAAGCTGGAACCTCTCTGAGCCCGGAGGCTCTCGGATG	525
QY	177	GlnGlnTyrLeuSer---GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeu	195
DB	526	ATAGATGGACACTTAAGCCGTTCTGTCGGGCATCACCACATGAGCTTCCCTTG	585
QY	196	SerSerHisProIleLeuGlyAspTyrSerIleGlnValGlnValAsnAspGlnThrTyr	215
DB	586	TCCGACCAAGCTGTGTGGAGAATGGTTCTATTTTGTGAATGCAAGGCCAGCGGTAC	645
QY	216	TyrGlnSerPheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThr	235
DB	646	AACAGTCTTTTGAAGTTCAAGATATGTGTGCCAAGTTTGAGCTTCTGATTGACCG	705
QY	236	ProLeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysThr	255
DB	706	CCCCGGTATATCCAAAGACCTCGACGCTGTGAGACAGGCACTGTGCGGGCCAGGTATAC	765
QY	256	TyrGlyLysProValLysGlyAsp-----ValThrLeuThrPheLeuProLeuSerPhe	273
DB	766	TTTGGAAACCTGTGGCTGTGCTTAATGATCAACATGACTGTTAATGGTGTAGGGTAC	825
QY	274	TrpGlyLysLys-----LysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsn	291
DB	826	TACAGCCAGAGTGGGAGCGCCCTGTCTCAGAACACCAAGATCTCTCGCTCCCGGAC	885
QY	292	PheSerPheAsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGlu	311
DB	886	TTCCACATCTCGTGAGGGACATG-----	909
QY	312	TyrLeuAspLeuSerSerPro-----GlyProValGluIleLeuThrVal	327
DB	910	---ATCCAGCGGAGCTCCCTGAGCACTTCGGGGGAGGTCAGCACTCGGCATCGTG	966
QY	328	ThrGluSerValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHis	347
DB	967	ACC---AGTGTGGACGGGAGCCAGCAG-----	990
QY	348	AspTyrIleIleGluPhePheAspTyrThrVal-----	359
DB	991	-----GTGCGTTCGATGACTCCACCCCTGAGAGCGAGCTGTGGACATCCGG	1041
QY	360	-----LeuLysProSerLeuAsnPheThrAlaThrValLys	371
DB	1042	TACTCAAGGACACGAGGAAGCAGTTCAGCGCGCTGGCTACGTGGGAGGTGGAG	1101
QY	372	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgArgAsnValValle	391
DB	1102	CTATCTACCCCGATGGCAGCCCA-----GCTAGGGGGTGCAGGTC	1143
QY	392	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	411
DB	1144	CAGATT-----	1152
QY	412	MetGluAlaValGlnLysIleAsn---TyrThr-----ValProGlnSerGlyThr	427
DB	1153	CGAGAGCTGACACCAAGGATACATCTACACCAAGTGAAGTGTGTCCCGCGTGGACTA	1212
QY	428	PheLysIleGluPheProIleLeuGluAspSerSerGlu-----LeuGlnLeuLys	444
DB	1213	GTGGGTTTGAATCCCTCCATCCACAGTCAGCCAGCAGCGTGTGGTGGACCAAG	1272
QY	445	AlaTyrPheLeuGlySerLys-----SerSerMetAlaVal	456
DB	1273	GTGATGGACATGAACGGGAGCCCGGTGGGCTCAGTACCTGCCCCAGCTACCTCTCCCTC	1332
QY	457	HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsn	476

Db 1333 GGCAGCTGGTAC---TCCCCAGCCAGTGTACTGTCAGCTGCAGCCACCCCTCCACCCA 1389  
Qy 477 IleLysValGlySerProPheGluLeuValValSerGlyAsnLysArgLeuLys---Glu 495  
Db 1390 CTCAGGTTGGGAAGAAGCCTATTTTCTGTGAAGTCCACATGTCCTCGCACTTTACC 1449  
Qy 496 LeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLysGln----- 512  
Db 1450 CTGTACTACAGGTGGCTGCACGGGCAATATTGTCTATCGGGCCAGCAGCCTGCCAC 1509  
Qy 512----- 512  
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Qy 513-----Asn 513  
Db 1570 CACCTTCTGAGACAGAGCCCCCACCAGCCCCAGAGCTGAGTGCAGCTGTGTGACC 1629  
Qy 514 SerThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleVal 533  
Db 1630 TCTTCTCATCTGCCCGTACCCCC-----AGCATGGTCCCTTGTGTCGCTGTGTC 1683  
Qy 534 TyrTyrIleGluAspGlyGluIleIleSerAspValLeuLysIleProValGlnLeu 553  
Db 1684 TTCTACGTACAGGAGATGAGAGGGGTGCCGACAGCCTTCAGTTTCAGTTCGAGACC 1743  
Qy 554 ValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLys 573  
Db 1744 TTCTTCGAAACCAACAGTTTCAGTGAAGTATTTCAGCAATGAGACCACCACTGGGAGGT 1803  
Qy 574 ValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaValAsp 593  
Db 1804 GTCCAGCTGGGATCAGGGCTGCAAG---GGCAGCTGTGTGTGCTGCCCGCAGTTGAT 1860  
Qy 594 LysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValValHisGlu 613  
Db 1861 AAGAGTGTCTACCTGTCTCAGGTCTGGGTTCCGGCTGACTCCTGCCCAGGTTTCCAGAA 1920  
Qy 614 LeuGluLeuTyrAsnThrGly----- 620  
Db 1921 CTGGAAGATTATGATGTTTCTGATCTCTTGGCGTGTCCAGGAGGATGTCCTTTTGG 1980  
Qy 621-----TyrTyrLeuGly 624  
Db 1981 TGGCTGGCTGACGGCACAAACACCGCGGCTCTCTGCTTCCCGTGGCTTGGGC 2040  
Qy 625 MetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAsp--- 643  
Db 2041 ATCACAAGGACTCTGGGTTTGGCTTTCACCGAAACGGGACTGTGTGTGATGACCGACGA 2100  
Qy 644 AlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyrAlaGluArg 663  
Db 2101 GTAGGCTGAACCCCGCAGGACGGTGGGCTCTAC-----ACCAGTGGCTGTCCCC 2154  
Qy 664 PheMetGluAsnGlnGluHisIleValAspIleHisAspPheSerLeuGlySerSer 683  
Db 2155 GCTTTCCAGCCCCACACAGGAGCGCTGTG-----GCAGTGGCTCCTTCC 2199  
Qy 684 ProHis-----ValArgLysHisPheProGluThrTrpIleTrp 696  
Db 2200 AGGCACCCCCCAGACAGAGAGAGAAAGAGACTTCTTCCCGAAACATGATTTCG 2259  
Qy 697 LeuAspThrAsnMetGlyTyrArgIleTyrGln---GluPheGluValThrValProAsp 715  
Db 2260 CATGTCTCAACATCAGTACCCTCTGTGGAGGACACATCAGTGTGAAGTCCCGGAC 2319  
Qy 716 SerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeu 735  
Db 2320 TCCATCACCAGCTGGGTGGGTGAGCGCGCTGTCCACCTCTCAGGCTTAGGCATC 2379  
Qy 736 ThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuPro 755

Db 2380 ---GCCGAGCCCTCCCTGCTGCTGAAGACCTTCAAGCCCTTCTTCGTGGACTTCATGCTCCCC 2436  
Qy 756 TyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLys 775  
Db 2437 GCTCTCATCATCCGTGGGAGCAGGTCAAGATCCCGCTCAGTCTACAACTACATGGC 2496  
Qy 776 AspAlaThrGluVal-----LysValIleIleGluLysSerAspLysPheAspIleLeu 793  
Db 2497 ACCTCGCTGAGGTGTACATGAAGCTCTCGGTGCCAAGGAGCATCCAGTTT----- 2547  
Qy 794 MetThrSerSerGluIleAsnAlaThrGlyHis-----GlnGlnThr 807  
Db 2548 -----GTTGGGCTCTCTGGCAACGCCATGTGACCAAGAG 2583  
Qy 808 LeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProThrHisLeu 827  
Db 2584 ATGTGTGGGCCCCCGGGAGGCTGAGCCATCTGGGTCTGTCTCTCTCCTCAGGACCTG 2643  
Qy 828 GlyGluIleProIleThrValThrAlaLeuSer----- 838  
Db 2644 GACTCAACAACATCACGGCCAAAGCCCTTCTTACGGAGACACAAATTGTCGCGGAT 2703  
Qy 839-----ProThrAlaSer 842  
Db 2704 GGGAGTCCAGCAACACCCCTGAGGAGATCACGCCGACAGGAGGTCCCATCGGGTG 2763  
Qy 843 AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln 862  
Db 2764 GATCAGCTCAGCGCAGTGTGATGTTGAGCGGAAGAGTCCCCCGGCGCTACACCTAC 2823  
Qy 863 SerIleLeu----- 865  
Db 2824 AGCGATTCTTCTGTCCAGTGAGAGTCCACATCTCCACCCCCACAAAGTATGATTC 2883  
Qy 866-----LeuAspLeuThr----- 869  
Db 2884 CAGTATGTGACGCGCCACCTGCGCTCACCGCTTGTGTGGTGTGCGAGCTCACAAT 2943  
Qy 870 AspAsnArgLeu----- 873  
Db 2944 GATGCCGTGTGGCCTTGTCTTCTGGGCCCCAGGACACAGCAGGATGATCGAGATGCTC 3003  
Qy 873----- 873  
Db 3004 CTGGGGGGGCATCAGAACACACAGGTGATGATCTCCACCAGAAAGATGGGAGAGCCGTG 3063  
Qy 874-----GlnSerThrLeuLysThrLeuSerPhe----- 882  
Db 3064 GCCAGTGACACACAGCGCCAAAGATCTCTCTCTGGGATGAATTTCAGAACATTCGATCAGC 3123  
Qy 882----- 882  
Db 3124 TGGCGTGTGGCTTATCCAGGTTGGCCATGGTCCAGAGCCATCCAAATGAGTCTGTCTATT 3183  
Qy 882----- 882  
Db 3184 GTGGCTGGAGCCCTCCCGAGGCCACAGAGGTCCAGTTTCAATGGCTTTTCCACCGGTGG 3243  
Qy 882----- 882  
Db 3244 GGCTCCATGGGTGAATTCGGAATCTGGAGGAAGATGGAGGTGGAGAGAGTACAGCGAG 3303  
Qy 883-----SerPheProAsnThrValThrGlySerGluArgValGlnIleThr 898  
Db 3304 GCCTTACCTCGGGGTCCACACGGCGCCATCCTCTGGTCTGAGCAGGACCCCGCTCC 3363  
Qy 899 AlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetPro 918  
Db 3364 ATCATCGGGAGCTCATGGGGCCAAACCCCTGAACACCTCAACACCTCTCTCGGGTCCG 3423  
Qy 919 TyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyr 938  
Db 3424 TTTGGCTGTGAGAGCAGAAACATGATCCACITTCACCCCAACGCTTGTCTTGAAGTAT 3483





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; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-198-25

Alignment Scores:
Pred. No.: 1,2e-142 Length: 6195
Score: 1529.50 Matches: 494
Percent Similarity: 40.87% Conservative: 258
Best Local Similarity: 26.85% Mismatches: 559
Query Match: 20.82% Indels: 529
DB: 16 Gaps: 57

US-10-020-095-4 (1-1428) x US-10-085-198-25 (1-6195)
QY 5 ProLeuLeuThrAlaAlaHisLeuLeuCysValCys-----ThrAlaAlaLeu 20
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QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyLeuLeuArgProGly 40
DB 82 CTTCAAGCCCGGGT-----TACTTGATTGAGCTCCCTCTGTTTTCGCGGCGGTG 135
QY 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60
DB 136 GAGGAGTATCATGAGTGACCACTTT---AATCTCCAGGAGTACAGTCCGTCAGGCT 192
QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGly---Val 79
DB 193 CAGCTGGTGGCCCGAGGTGAG-----CCGGTGGTGAGAGCCAGGAGGCATC 240
QY 80 PheGluLysGlySerPheLys-----86
DB 241 CTGGATAAAGGGAACAATCAAACTCAAGCATACGCTCTCAGCACCTCCGGTATCTCCCTC 300
QY 87 -----ThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyr 102
DB 301 CTGCCCATCTTCCCTCTCTTGGTGGCGGAGCTTTCTCTCTCTCTCAGCCTCTGG 360
QY 103 Glu-----103
DB 361 CCAGTGTTCAGATATTCCAGAAACAGGCGCAGGTGCCACGCGCTCCGCGGCCAAGCG 420
QY 104 ---LeuArgValThrGlyArg-----ThrGlnAspGluIleLeuPheSerAsnSer 119
DB 421 CTTCTGAAGTGTGGGCGCCGCGCTGGAGCGGAGGAGGGGCCCTCTTTCACACACAG 480
QY 120 ThrArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeu 139
DB 481 ACCTCGTGACCGTGAGCGCGCGCGGCGCTCTGTATTATCATCAGACGACGACAAAGCTGTG 540
QY 140 TyrLysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysPro 159
DB 541 TACAGACCCGAGCAGCGAGTGCTCAAGACATCTTCACCGCTCTCTCCAAATCTGAGGCT 600
QY 160 TyrLysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnIntTrp 179
DB 601 GTCAACGAGAAGCTGGAAGCCTATCTCTGACACCCCGAGGCTCTCGGATGATAGATGG 660
QY 180 LeuSer---GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHis 198
DB 661 AGACACTTAAAGCGGTCTCTCGCGCATCATCAACATGAGCTTCCCTCTGTCGACACAG 720
QY 199 ProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSer 218
DB 721 CTTGTGTGGGAAGTGGTTTCAATTTTGTGAATGCAAGGCCACCGGTACACAGTCT 780
QY 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyr 238
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DB 781 TTTGAAGTTCAGAAAGTATGTGTTCCCAAGTTTTCAGGCTTCTGATTGACCCCGCGGTAT 840
QY 239 CysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLys 258
DB 841 ATCCAAGACCTGGACCGCTGTGACAGAGGCACTGTGCGGCGCACGTATACCTTTGGGAAA 900
QY 259 ProValLysGlyAsp-----ValThrLeuThrPheLeuProLeuSerPheTrpGlyLys 276
DB 901 CTTGTGGCTGGTCTTAATGATCAATGACTTAAATGGTGTAGGTACTACAGCCAC 960
QY 277 Lys-----LysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPhe 294
DB 961 GAGGTGGACGCCCTGTCTCAGAACCAACCAAGATCTCTCGGCTCCCGGACTTCGACATC 1020
QY 295 AsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAsp 314
DB 1021 TCGGTGAGGACATG-----ATCCCA 1041
QY 315 LeuSerSerPro-----GlyProValGluIleLeuThrValThrValThrGluSer 330
DB 1042 CGGACGCTCCCTGAGCACTTCCGGGCGAGGCTCAGCATCTGGGCATGCTGACG---AGT 1098
QY 331 ValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIle 350
DB 1099 GTGACGGGAGCCAGCAG-----1116
QY 351 IleGluPhePheAspTyrThrVal-----359
DB 1117 GTCGGTTCGATGACTCCACCCCGTCAGAGCGAGCTGGTGGACATCCGGTACTCCAAAG 1176
QY 360 -----LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArg 374
DB 1177 GACACGAGAAAGCATTTCAAGCCGGGCTGCTACGTGGGGAAGGTGGAGCTATCTCTAC 1236
QY 375 AlaAspGlyAsnGlnLeuThrLeuGluArgAsnValIleThrValThr 394
DB 1237 CCCGATGACGCCCA-----CCTGAGGGGTGACGCTCCAGATT---1275
QY 395 GlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMerGluAla 414
DB 1276 -----AAGGCAGAGCTG 1287
QY 415 ValGlnLysIleAsn---TyrThr-----ValProGlnSerGlyThrPheLysIle 430
DB 1288 ACACAAAGGATAACATCTACACAGTGAAGTTGTGCCAGCGTGACTAGTGGGTTT 1347
QY 431 GluPheProIleLeuGluAspSerSerGlu-----LeuGlnLeuLysAlaTyrPhe 447
DB 1348 GAATCCCTCCATCCCACTGAGCCAGCACGCTGCTGGAGACCAAGGTGATGCA 1407
QY 448 LeuGlySerLys-----SerSerMetAlaValHisSerLeu 459
DB 1408 CTGAACGGGAAGCCCGTGGGGGCTCAGTACCTGCCACGACTACCTCTCCCTCGGAGCTGG 1467
QY 460 PheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysVal 479
DB 1468 TAC---TCCCCAGCCAGTGTACTGAGCTGAGCCACCCCTCCACCCACTGCAGTT 1524
QY 480 GlySerProPheGluLeuValValSerGlyAsnLysArgLeuLys---GluLeuSerTyr 498
DB 1525 GGGGAAGAAGCCTATTTTCTGTGAAGTCCACATGTCTCTGCAACTTTTACCTGTACTAC 1584
QY 499 MetValValSerArgGlyGlnLeuValAlaValGlyLysGln-----512
DB 1585 GAGGTGGCTGACCGGGGCAATATTGTGTATCGGCGCAGCAGCTGCCACACCCACCGAG 1644
QY 512 -----512
DB 1645 CAGCGAAGCAAGCGGGGCGCCCTGCTCGTGGAGAAACCGATTCTGTTTAAACACACTTCT 1704
QY 513 -----AsnSerThrMet 516
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; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 4492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4374)
US-10-096-625-199

Alignment Scores:
Pred. No.: 2,64e-134 Length: 4492
Score: 1444.50 Matches: 431
Percent Similarity: 44.28% Conservative: 273
Best Local Similarity: 27.11% Mismatches: 571
Query Match: 19.66% Indels: 315
DB: 13 Gaps: 46

US-10-020-095-4 (1-1428) x US-10-096-625-199 (1-4492)
Qy 20 LeuAlaValAlaProGly-----ProArgPheLeuValThralaProGly 34
Db 28 TTGGCCCTATCACCAGCATTGGCAGAGAACTTCCAAACTACCTGGTGACATTACCAGCG 87
Qy 35 IleIleArg---ProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHisCysPro 53
Db 88 CGGTAAATTTCCCTC-----TCCGTTCAAGAGGTTTGTGTGGACCTGAGCCCT 135
Qy 54 SerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrValSerVal 73
Db 136 GGTACAGTGATGTTAAATTTACCGGTTACTCTGGAGACCAAGGACCAAGCCAGAGTTG 195
Qy 74 LeuGluAlaGluGlyValPheGluLysGlySerPheLysThrLeuThrLeuProSerLeu 93
Db 196 CTAGATACTCTGGACTGAAGAGAGAGGCACTTACATTGTATCTCTTCTGTACCACT 255
Qy 94 ProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThrGlyArgThrGlnAspGlu 113
Db 256 CTGCTGGTGGCACAGAAAGAGTGGCCCACTCGGGTGTGGGA---GTTGGAATAAC 312
Qy 114 IleLeuPheSerAsnSerThrArgLeuSerPheGluThrLysArgIleSerValPheIle 133
Db 313 ATCAGCTTTGAGGAGAAAGAAAGGTTCTAATTCAGAGGAGGAGGAAACGCGACCTTTGTA 372
Qy 134 GlnThrAspLysAlaLeuTyrLysProLysGlnLysValLysPheArgIleValThrLeu 153
Db 373 CAGACTGACAAACCTCTCTACCCAGGCGAGCAAGTGATTTCCGCAATGTCCACATG 432
Qy 154 PheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu---IleLysAspProLys 172
Db 433 GATAGCAACTTCGTTCCAGTGAATGACAACTACTCCATGTGTGGAATACAGGATCCAAAT 492
Qy 173 SerAsnLeuIleGlnGlnThrLeuSerGlnSerAspLeuGlyValIleSerLysThr 192
Db 493 AGCAACAGGATTCACAGATGGGTGAAGTGGTACCTGAGCAAGGCAATGTGACCTGCTCC 552
Qy 193 PheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAsp 212
Db 553 TTCCAACCTGGCACCAGAGGCAATGCTGGCACCTACACT-----GTGGCAGTGGCTGAG 606

213 GlnThrTyrTyrGlnSerPheGlnValSerGluTyr----- 224
Db 607 GGCAAGACCTTTGTGTACTTTTCAGTGTGGAGCAATATGTCTTCTCCATTTCCTCTTTA 666
Qy 225 -----ValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMet 241
Db 667 CTCCTCTTCAGTGCCTGCCGAGTTTAAAGTGAAGTGGTGAACCAAGGAGTATATCAAG 726
Qy 242 AsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLys 261
Db 727 GTGCAGGAATCTTCTTAGTAAATTTGTGTAGGTACACCTATGCAAGGCCATCTGCTA 786
Qy 282 GlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnIleThr 281
Db 787 GGGCAGTGCAGGTATCTGTGTGT-----CAGAAGGCAAT----- 822
Qy 282 LysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLysAsn 301
Db 823 -----ACTTACTGGTATCGAGAGGTGGACGGGAACAG 855
Qy 302 ValMetAspSerSerAsnGlyLeuSerGluTyrLeuAsp-----LeuSerSer 317
Db 856 CTTCTGACAAATGCAGGAACCTCTCTGGACAGACTGACAAACACAGGATGTTTCTCAGCA 915
Qy 318 Pro-----GlyProValGluIle 323
Db 916 CCGTGGACATGGCCACCTTTGACCTCATTTGGATATCGGTACAGCCATCAATATATT 975
Qy 324 LeuThrValThrGluSerValThrGlyIleSerArgAsnValSerThrAsnValPhe 343
Db 976 GTGGCTACTGTGTGGAGGAAGGACAGAGTGTGGAGGCCAATGCCACTCAGATATCTAC 1035
Qy 344 PheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeuLysProSer 363
Db 1036 ATTTCTCCAAATGGGATCAATGACCTTTGAAGACACACAGCAATTTTACCATCCAAAT 1095
Qy 364 LeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGlu 383
Db 1096 TTCCCTTCAGTGGGAGAGTCTCTCAAGTTTCCGCAAGGCGGTGTCTCCCTTGGCAAG 1155
Qy 384 GluArgArgAsnValValIle-----ThrVal 393
Db 1156 AACCATCTAGTGTCTTCTGGTGATTTATGGCACAATGAAACCTTCAACCAACCCCTGGT 1215
Qy 394 ThrGlnArgAsn-----TyrThrGluTyrTrpSerGlySerAsn 406
Db 1216 ACTGATACAATGGCCTAGCTCCCTTTACCTTGGAGACATCCGGTGGATGGACAGAC 1275
Qy 407 SerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGly 426
Db 1276 -----GTTTCTCTGGAGGGA 1290
Qy 427 ThrPheLysIleGlu-----PheProIleLeuGluAspSer 438
Db 1291 AAGTTTCAATGGAGACTTAGTATATAATCCGGAACAAGTGCACCGTACTACTACCAAT 1350
Qy 439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458
Db 1351 GCCTACCTGCACCTGGACCCCTTCTACAGCACAACCCGACAGTCTCTTGGCATCCACCG 1410
Qy 459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478
Db 1411 CTA-----AACGCCCTTGGAA 1428
Qy 479 ValGlySerProPheGluLeuValVal-----SerGly 489
Db 1429 TGTGCCAGCCCCAGGAAGTCTGTGTGATTATTATTCGACCCCGCGGATGCAAGCCCT 1488
Qy 490 AsnLysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaVal 509
Db 1489 GACCAAGAGATC---AGCTTCTCTACTATTATTAAGGAAGGAAGTTTGGTATGAG 1545
Qy 510 GlyLysGlnAsn-----SerThrMetPheSerLeu 519

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Db	1546	GGGCAGAAACACCTGAACTCTAAGAGAAAGGACTGAAGCCCTCTTCTCTCTCTCACTG	1605
Qy	520	ThrProGluAsnSerTprThrProLysAlaCysValIleValTyTrpIleGluAspAsp	539
Db	1606	ACCTTCACTTCGAGACTGGCCCTGATCCTTCCCTGGTGATCTATGCCATTTTCCCACT	1665
Qy	540	GlyCluIleLeuSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIle	559
Db	1666	GGAGGTGTTPAGCTGACAAATTCAGTCTTCAGTCGAGATGTGCTTTGACAAT----	1719
Qy	560	LysLeuTyTrpSerLysValLysAlaGluProSerGluLysValSerLeuAtgIleSer	579
Db	1720	-----CAGCAGCTTCCAGGACGAGAGTGGAGCTGCAGCTGCAG	1758
Qy	580	ValThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMet	599
Db	1759	GCAGCT---CCCGATCCCTGTGTGCCTCCGGCGGTGGATGAGATGTCTTACTGCTT	1815
Qy	600	AsnAlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyAsnThr	619
Db	1816	AGGCCA-----GACAGAGAGCTGAGCAACCGC	1842
Qy	620	GlyTyrTyrLeuGlyMetPhe-----	626
Db	1843	TCTGTCTAT---GGGATGTTTCCATTCTGGTATGGTCACTACCCCTATCAAGTGGCTGAG	1899
Qy	626	-----	626
Db	1900	TATGATCAGTGTCCAGTGTCTGGCCCATGGGACTTTCCTCAGCCCTCATTTGACCCAAATG	1959
Qy	627	-----Met	627
Db	1960	CCCCAAGGCATTCCAGCCAGCTTCCATTATCTGGAGGCCCTCGTTCTCTGAAGGCACG	2019
Qy	628	AsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThr	647
Db	2020	GACCTTTTCAGCTTTTCCGGAGCTGGCGTGAATACTGTCCAATGCCAAATCAAG	2079
Qy	648	LysAspTyrIleAspGlyValTyTrpAspAsnAlaGluTyAla-----	661
Db	2080	AAGCCA---GTAGATTCCAGTCACAGATCCAGAAATACAGCACTGCTATGGTGGCGGT	2136
Qy	662	-----GluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPhe	678
Db	2137	GGTCATCCAGAGGCTTTTGATGTCATCAACTCTTTTACATCAAGCAGAG-----	2184
Qy	679	SerLeuGlySerSerProHisValArgLysHisPheProGluThrTrpIleTyrLeuAsp	698
Db	2185	-----GATTCTCAGTCCGCCAGTACTTCCAGAGACCTGGCTCTGGGATCTG	2232
Qy	699	ThrAsnMetGlyTyArgIleTyGlnGluPheGluValThrValProAspSerIleThr	718
Db	2233	TTTCCTATTGTAACTCGGGAAGAGGCGGTCCACGTCACAGTTCCTGACGCCATCACC	2292
Qy	719	SerTrpValAlaThrGlyPheValIleSerCluAspLeuGlyLeuGlyLeuThrThr	738
Db	2293	GAGTGAAGGCGATGAGTTTCTGCATTTCCAGTCCAGAGCTTCGGGCTTTCACCCACT	2352
Qy	739	ProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyTrpSerVal	758
Db	2353	---GTTGGACTAACTGCTTTCAAGCCGTTCTTTGTTGACCTGACTCTCCCTTACTCAGTA	2409
Qy	759	IleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyLeuLysAspAlaThr	778
Db	2410	GTCCGTGGGAATCCTTTCGTTCTTACTGCCACCATCTTCAATTAACCTAAAGGATTCATC	2469
Qy	779	GluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGlu	798
Db	2470	AGGTTTCAGACTGACCTGGCTTAATTCGATGAGTACCAGCTAGTAATCATGGGACATTCT	2529
Qy	799	IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrVal	818

2530	Db	-----CAGACCTCAGTTGCTCTGTGCTGATGAGCGMAAAACCCAC	2571
819	Qy	LeuPheProIleArpProThrHisLeuGlyGluIleProIleThrValThrAlaLeu---	837
2572	Db	CACTGGCAATCATCAGAGCTGTCAAATTGGGTACACATTAACTTACTATTAGTACAAAGATT	2631
838	Qy	-----SerProThrAlaSer	842
2632	Db	CTGGACAGCAATGAACCATGTGGGGCCAGAGGGTTTGTTCCTCCCAAAAGGCCGAAGT	2691
843	Qy	AspAlaValThrGlnMetIleLeuValIleAlaGluGlyIleGluLysSerTyrSerGln	862
2692	Db	CACACGCTCATCAAGCCAGTTCTCGTCAAACTGAGGAGTCTCTGTGGAGAGACACAC	2751
863	Qy	SerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeuSerPhe	882
2752	Db	AGCTCATGTCTGCCCAAAAGGAGGAAGTGGCATCT-----GAATCTGTCTCCCTG	2805
883	Qy	SerPheProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAsp	902
2806	Db	GAGCTCCAGTGGACATTGTTCTCTGACTCGACCAAGGCTTATGTACGGTCTCTGGAGAC	2865
903	Qy	ValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGly	922
2866	Db	ATTATGGGCACAGCCCTCGCAACCTCGATGGTCTGTGCAGATGCCACGTGGCTGTGGC	2925
923	Qy	GluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThrLysLys	942
2926	Db	GAGCAGAACATGGTCTTGTGTCTCCCATCATCTATGTCTTGAGTACTTGGAGAGGCCA	2985
943	Qy	LysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGlyTyrGln	962
2986	Db	GGGCTGTGACGGAGGAGATCAGGTCTCGGCGAGTGGTTCCTGGAAATAGGGTACCA	3045
963	Qy	ArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspPro	982
3046	Db	AAGAGCTGATGTACAAACACAGCAATGGCTCATACAGTGCCTTGGGAGCCAGATGGA	3105
983	Qy	SerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyr	1002
3106	Db	AATGGAAACACATGCTGACAGCGTTTGCACAAATGCTTGSCCAAGCTCAGAAATTC	3165
1003	Qy	IleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGlnLys	1022
3166	Db	ATCTTCATGTATCCCAAGAACATCCAGGATGCTCTCAAGTGGATGGCAGAAACCACTC	3225
1023	Qy	SerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGlyAsn	1042
3226	Db	CCCAGTGGCTGATGCCACGTCGGAAATCTCCTTCACACAGCTATGAGGGTGGTGT	3285
1043	Qy	LysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLysTyr	1062
3286	Db	GATGATGAGGTCTCCTTGACTGCGTATGTCACAGCTCATTTGTTGGAGATGGGAAGGAT	3345
1063	Qy	GlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGly	1082
3346	Db	GTAGATGACCAATGTTGAGTCAGGCTCAGGGTGTCTCAAGAAATCG-----GCCACCTCC	3402
1083	Qy	IleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerPro	1102
3403	Db	ACGACCAACCTCTACACAGCGCCCTGTTGGCTTACATTTTCTCCCTGGCTGGGAAATG	3462
1103	Qy	LysAlaLysGlu---AlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyGlyMet	1121
3463	Db	GACATCAGAAACATCTTCCTTAAACAGTTATGATCAACAGGCTATCATCTCAGAGAAATCC	3522
1122	Qy	GlnPheTrpValSerSerGluSerLysLeuSerAspSer-----Trp---GlnProArg	1138
3523	Db	ATTTACTGGAGCCAGAAACCTACTCCATCATCGAACCCAGCCCTTGCTGTGAGCTGCG	3582
1139	Qy	SerLeuAspIleGluValAlaAlaTyrAlaLeuLeuSerHis-----Phe	1153
3583	Db	GCTGTAGATGGAACTCAGAGATATGCATTTGTTGCCCGAGCTTACACAGCCACGCTG	3642

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Qy 1154 LeuGlnPheGlnThrSerGluGluIleProIleMetArgTrpLeuSerArgGlnArgAsn 1173
Db 3643 ACTCAAGAGAGATGAGCAAGCCATAGCATAGTGGCTTGGTGGCAAGCAACAAT 3702
Qy 1174 SerLeuGlyGlyPheAlaSerThrGlnAspThrValAlaLeuLysAlaLeuSerGlu 1193
Db 3703 GCATATGGGGCTCTCTTCTACTCAGACACTGTAGTGTCTCCAAAGCTTGGCAAA 3762
Qy 1194 PheAla-----AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThr 1210
Db 3763 TATGCCACTACCGCTACATGCCATCTGAGGAGATCAACCTGTGTGTAAATCCACTGAG 3822
Qy 1211 -----GlyProSerSerProSerProLeuAlaValValGln----- 1222
Db 3823 AATTCACGGCCACATTCACATACATACAGTCAGTTACAGATTTGTATTTACAGAGGATACC 3882
Qy 1223 -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
Db 3883 CTGCCCAATGTCCCTGGAATGTACACGTTCGAGGCTCAGGCCAGGCTGTGTCTATGTG 3942
Qy 1239 GlnLeuAsnValValThrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258
Db 3943 CAGACGGTGTGTGAGATACATATCTCCCTCCC----- 3975
Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLys 1274
Db 3976 ACAATATGAGACCTTTAGTCTTAGTGTGGAATAGAAAGCTAGATCTGAGCAGCCG 4035
Qy 1275 AspAspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyPro---GlyArg 1293
Db 4036 ACTTCACCTCGATCTCTGACTCTCACTATTCACACCATGATATGTGGGGAGCCGTACTCT 4095
Qy 1294 SerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPhe-----MetValProSer 1311
Db 4096 TCCATATGCTATGTGGAAGTGAAGATGCTATCTGGTTTCAGTCCCATGGAGGCCACC 4155
Qy 1312 GluAlaIleSerLeuSerGlu---ThrValLysValGluIleValAspHisGlyLysLeu 1330
Db 4156 AATCAGTTACTTCTCCAGCAACCCCTGCTGAAGAAGGTTGAATTTGGAAGTACACACTT 4215
Qy 1331 AsnLeuTyrlleuAspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArg 1350
Db 4216 AACATTTACTTGGATGATGCTCAATTAAGAACCTCAGACTTACACCTTCCACTACGCCAA 4275
Qy 1351 AsnPhelysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrlleuPro 1370
Db 4276 AGTGTGCTGCTCACCACCTTGAACCCAGCAACCATCAAGTCTATGACTACTACCTACCA 4335
Qy 1371 ArgArgGlnAlaValArgSerTyrlleuSer-----GluVal 1382
Db 4336 GATGAACAGCAGCAACAATTCAGTATCTTCATCCCTGTGAATGAGGATAGGAGCTGGAATC 4395
Qy 1383 LysLeuSerSerCysAspLeuCysSerAspValGlnGlnGlyCysArgProCysGluAspGly 1402
Db 4396 CAATTAGTCTCTGTGACATTTACTGGAGGTGGAA----- 4431
Qy 1403 AlaSerGlySerHisHisSerSerVal 1412
Db 4432 -----CATTTCTTGTCTC 4443

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## RESULT 10

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US-10-608-397-7
; Sequence 7, Application US/10608397
; Publication No. US20040067512A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth David Becker
; APPLICANT: Gonul Velicelebi
; APPLICANT: Xin Wang
; APPLICANT: Rudolph E. Tanzi
; APPLICANT: Lars Bertram
; APPLICANT: Aleister J. Saunders
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLOB

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; FILE REFERENCE: 37481-3323B
; CURRENT APPLICATION NUMBER: US/10/608,397
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/292,081
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/337,434
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4576
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-608-397-7

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Alignment Scores:
Pred. No.: 6,15e-134 Length: 4576
Score: 1441.00 Matches: 453
Percent Similarity: 46.20% Conservative: 264
Best Local Similarity: 29.19% Mismatches: 551
Query Match: 19.61% Indels: 284
DB: 13 Gaps: 60

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US-10-020-095-4 (1-1428) x US-10-608-397-7 (1-4576)

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Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31
Db 85 CTCITGGTCTCTCTGCCACAGCGCTCAGTCTCTGGAACCGCAGTATATGTTCTG 144
Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuGluHis 51
Db 145 GTCCCTCTCTCTCCACACT---GAGACCACTGAGAAGGGCTGTGTCTTCTGAGTAC 201
Qy 52 CysProSerGlnValThrValLysAlaGluLeuLysThrAlaSerAsnLeuThrVal 71
Db 202 CTGAATGAGACAGTACTGTGAAGTCTTCTTGGAGTCTGTCCAGGGGAAACAGGAGCCTC 261
Qy 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
Db 262 TTCATCTGCTGGAGGGGAGAGATGAGTACTCCACTGTGTGCGCTTC--- 309
Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrlleuArgVal 106
Db 310 -----GCTGTCCCAAGTCTTCATCCAGGAGAGTAAATGTCTCCTCAGTCCCAAGTG 363
Qy 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
Db 364 AAAGACCAACCCCAAGAA-----TTTAAAGAGCGGACCAACAGTGTGTTAAGAAC 414
Qy 127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrlleuLysProLysGlnVal 146
Db 415 GAGGACAGCTGTGCTTTGTCCAGACAGACAAATCAATCTACAAACCCAGGCGACAGTG 474
Qy 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrlleuSerLeuAsnIle 166
Db 475 AAATTCGTGTGTCTCCATGATGAAACATTTTCCACCCCTGATGATGATGATGATGATGAT 534
Qy 167 Leu---IleLysAspProLysSerAsnLeuIleGlnThrPheSerGlnGlnSerAsp 185
Db 535 GTATACATTCAGGATCCCAAGGAAATCGCATCCCAATGGCAGAGTTTCCAGTTAGAG 594
Qy 186 LeuGlyValIleSerLysThrPheGlnLeuSerHisProIleLeuGlyAspTrpSer 205
Db 595 GGTGGCTCAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGGCTCCTACAAG 654
Qy 206 IleGlnValGlnValAsnAsp-----GlnThrTyrlleuSerPheGlnValSerGlu 223
Db 655 GTGGTGGTACAGAAAGAAATCAGGTGGAGGACAGAGCAC---CCTTTCCCGTGGAGGAA 711
Qy 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrlleuTyrlleuSerMetAsnSer 243
Db 712 TTTGTTCTTCCCAAGTTTGAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 771

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Db 2713 CCTGAACACGGAAGAAAGACACAGTCATCAAGCCCTCTGTGTGGTTGAACCTGAAGGACTA 2772  
 Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876  
 Db 2773 GAGAAGGAACAACATTCACCTCCCTACTTTTGCATCAGGTGGTGGAGTTTCT----- 2826  
 Qy 877 LeuLysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln 896  
 Db 2827 --GAAGATTATCCCTGAACCTCCACCAATATGTGTAGAGAATCTGCCGAGCTTCT 2883  
 Qy 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916  
 Db 2884 GTCTCAGTTTGGGAGACATATTAGGCTCTGCATGCAAAACACACAAAATCTTCCAG 2943  
 Qy 917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936  
 Db 2944 ATGCCCTATGCTGTGGAGAGCAGATATGGTCTCTTGTCTCTAACATCTATGACTG 3003  
 Qy 937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956  
 Db 3004 GATATCTAAATGAACACACAGCAGCTTACTCCAGAGATCAAGTCCCAAGGCCATTTGCTAT 3063  
 Qy 957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976  
 Db 3064 CTCAACACTGGTTTACACAGACAGATTGAACACTCAACACTATGATGGCTCTTACAGCAC 3123  
 Qy 977 PheGly---AsnTyrAspProSer---GlySerThrTriPheSerAlaPheValLeuArg 994  
 Db 3124 TTTGGGAGCGATATGCGACGACCAAGGCAACACCTGGCTCACAGCCCTTGTCTTGAAG 3183  
 Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014  
 Db 3184 ACTTTTCCCAAGCTCGAGCTCATCTTTCATCGATGAAGCACACATCAACCAAGCCCTC 3243  
 Qy 1015 ThrTriPheLysGlyHisGlnLysSerAsnGlyGluPheTyrAspProGlyArgValIle 1034  
 Db 3244 ATATGGCTCTCCAGAGCGAGAGGACATGGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3303  
 Qy 1035 HisSerGluLeuGlnGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054  
 Db 3304 AACAATGCCATAAAGGAGGAGTAGAAGATGAAGTGAAGTCCCTCTCCGCTATATCACCATC 3363  
 Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074  
 Db 3364 GCCCTCTGGAGATCTCTCACAGTCACCTGCTGTGTCGCAATGCCCTGTTTGC 3423  
 Qy 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088  
 Db 3424 CTGGAGTCAGCTGGAAGACAGCACAAAGAGGGGACCATGGC---AGCCATGTATATACC 3480  
 Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107  
 Db 3481 AAAGCACTGTGGCTATGCTTTTGGCTCGCGAGTAACCGAGACAGAGGAAGTA 3540  
 Qy 1108 LeuAsnMetLeuThrTyrPArgAlaGluGlnGlyMetGlnPheTrp----- 1124  
 Db 3541 CTCAAGTCACCTTAATGAGGAAGCTGTGAAGAAAGACAACTCTCTCCATTGGGAGCCCTC 3600  
 Qy 1125 ValSerSerGluSerLysLeuSerAspSerTyrGlnProArg-----SerLeuAspIle 1142  
 Db 3601 CAGAAACCCAGGACACAGTGGGCGCATTTTTCAGAACCCCGAGCTCCCTCTGTGAGGTG 3660  
 Qy 1143 GluValAlaAlaTyrAlaLeuSerHisPheLeuGlnPheGln-----ThrSer 1159  
 Db 3661 GAGATGATCCCTATGTCTCTCGCT---TATCTCAGCGCCCGAGCGCCCAACTCG 3717  
 Qy 1160 GluGlyIlePro-----IleMetArgTriPheSerArgGlnArgAsnSerLeu 1175  
 Db 3718 GAGGACCTGACCTCTGCAACCAACATCTGTGAAGTGGATCACGAAGCAGCAGATGCCAG 3777  
 Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195  
 Db 3778 GCGCGTTTCTCTCCACCCAGGACACAGTGTGGCTCTCCATGCTGTGTCCAAATATGA 3837

Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215  
 Db 3838 GCAGCCACATTTACC---AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3894  
 Qy 1216 SerProLeuAlaValValGln----- 1222  
 Db 3895 ACATTTTCCAGCAAAATTCCAAGTGGACAAACAAACCGCCTGTTACTGACAGAGGTCTCA 3954  
 Qy 1223 -----ProMetAlaValAlaSerAlaAsnGlyPheGlyPheAlaIleCys 1238  
 Db 3955 TTGCCAGAGCTGCTGGGAATACAGCATGAAAGTGCACAGGAGAGGATGTGTCTACCTC 4014  
 Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258  
 Db 4015 CAGACATCTTTGAAATACAATATT-----CTC 4041  
 Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275  
 Db 4042 CCAGAAAGGAGAGTTCCTCTTCTTTAGGAGTGAGACTCTGCCCTCAAACCTGTGTAT 4101  
 Qy 1276 AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly----- 1292  
 Db 4102 GAACCCAAAGCCACACAGCCTTCCAAATCTCCCTAAGTGTCACTTACACAGGAGCGCGC 4161  
 Qy 1293 ---ArgSerGlyMetAlaLeuMetGluValAsnLeuSerGlyPheMetValProSer 1311  
 Db 4162 TCTGCCCTCCAACTGGCGATGCTGTATGTAAGATGCTCTGGCTTCATTCCTCCTGAAG 4221  
 Qy 1312 GluAlaIleSerLeu-----SerGluThrValLysLysValGluTyrAspHisGly 1328  
 Db 4222 CCAACAGTGAAGATGCTTGAAGATCTTAACATGTGAGCGGACAGAGTGCAGCAGCAAC 4281  
 Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348  
 Db 4282 CATGCTGTGATTTACCTTGATAGTGTCAAGTGTCAAAATCAGACACTGAGCTTGTCTCACG 4341  
 Qy 1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368  
 Db 4342 CTGAAGATGTCCAGTAAGATCTGAACACGACCATAGTGAAGTCTATGATTACTATC 4401  
 Qy 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380  
 Db 4402 GAGACGGATGAGTTTGAATGTCTGAGTACAATGCT 4437

## RESULT 11

US-10-292-081A-7  
 ; Sequence 7, Application US/10292081A  
 ; Publication No. US20030162202A1

## GENERAL INFORMATION:

; APPLICANT: Kenneth David Becker  
 ; APPLICANT: Gonul Velicelebi  
 ; APPLICANT: Xin Wang  
 ; APPLICANT: Randolph E. Tanzi  
 ; APPLICANT: Lars Bertram  
 ; APPLICANT: Aigister J. Saunders  
 ; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLOB  
 ; FILE REFERENCE: 37481-3323  
 ; CURRENT APPLICATION NUMBER: US/10/292,081A  
 ; CURRENT FILING DATE: 2002-11-08  
 ; PRIOR APPLICATION NUMBER: 60/337434  
 ; PRIOR FILING DATE: 2001-11-09  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 4576  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

## US-10-292-081A-7

Alignment Scores:  
 Pred. No.: 6,15e-134 Length: 4576  
 Score: 1441.00 Matches: 453



Percent Similarity:	46.20%	Conservative:	264
Best Local Similarity:	29.19%	Mismatches:	551
Query Match:	19.61%	Indels:	284
DB:	15	Gaps:	60
US-10-020-095-4 (1-1428) x US-10-292-081A-7 (1-4576)			
QY	12	LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr	31
DB	85	CTCTTGCTCTCTGCCCCAGACGCTCAGTCTCTGGAAACCCGAGTATATGTTCTG	144
QY	32	AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis	51
DB	145	GTCCCTCTCTCTCCACACT---GAGACCACTGAGAAGGCTGTCTCTCTGAGCTAC	201
QY	52	CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuVal	71
DB	202	CTGAATGAGACAGTGTAGTCTTCTCTGAGTCTGTCTGAGGAAACACAGGAGCTC	261
QY	72	---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr	89
DB	262	TTCACTGACTGGAGCGGAGATGAGTACTCTCACTGTCTGCTCTC---309	
QY	90	LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal	106
DB	310	-----GCTGTCCCAAGTCTTCATCCATGAGGAGTAATGTTCTCTCACTGTCCAAGTG	363
QY	107	ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr	126
DB	364	AAAGGACCAACCCCAAG-----TTTAAGACGGGACACAGATGATGTTGAAGAC	414
QY	127	LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrIleProLysGlnGluVal	146
DB	415	GAGGACAGTCTGTCTTTGCCAGACAGACAATCAATCTACAAACCCAGGGCAGACAGTG	474
QY	147	LysPheArgIleValThrLeuPheSerAspPheLysProTyrIysThrSerLeuAsnIle	166
DB	475	AAATTTCTGTCTCTCCATGGATGAAACTTTCACTCCCTGAAATGAGTTGATTCACCTA	534
QY	167	Leu---IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnGlnSerAsp	185
DB	535	GTATACATTCAGATCCCAAGAAATCGCATCGCAATGGCAGAGTTTCAGTTAGAG	594
QY	186	LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer	205
DB	595	GGTGGCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGCTCTCTACAG	654
QY	206	IleGlnValValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu	223
DB	655	GTGGTGTACAGAAAGAAATCAGGTGGAGGACAGACAC---CCTTTCCACCGTGGAGAA	711
QY	224	TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer	243
DB	712	TTTGTCTTCTCCCAAGTTTGAAGTACAAGTACAAGTCCCAAGATAATCACCATCTGGAA	771
QY	244	LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp	263
DB	772	GAAGAGATGAATATATCATGTGTGTCCTATACACATATGGGAAGCTCTCTCCCTGACAT	831
QY	264	ValThrLeuThrPheLeuProLeu-----271	
DB	832	GTGACTGTGAGCAATTTGCAGAAAGATATAGTACGCTTCCGACTGCCACCGTGAAGTTCA	891
QY	272	-----SerPheTrpGlyLys	276
DB	892	CAGGCTTCTGTGAGAAATTCAGTGACAGCTAAACAGCCATCGGCTCTCTCATCAGCAA	951
QY	277	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp	296
DB	952	GTAAAA-----ACCAAGGTCTTCCAGCTGAAGAG-----AAGGAG	987
QY	297	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	316
DB			
988	TATGAATGAAA-----CTTCACACTGAGGCCAGATCAA	1023	
317	SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal	331	
1024	GAAGAAGGACAGTGGTGAATTCAGTGAAGGAGGAGTCCAGTGAATATCAACAAGAACATA	1083	
332	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle	351	
1084	ACCAACTCTCA---TTTGTGAAGTGAAGTCAACACTTTTCACAGGA-----ATT	1131	
352	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	371	
1132	CCCTTCTTTGG-----CAG	1146	
372	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgArgAsnAsnValValIle	391	
1147	GTGGCTCTAGTAGATGGAAAGCGTCCCTATATCA-----AATAAAGTACATA	1194	
392	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	411	
1195	TTCATC---AGAGGAATGAAGCAACTATTAC-----TCCATGTCTACACCGATGAG	1245	
412	MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe	428	
1246	CATGGCTTTGACAGTTCTCTATCAACACCACTAATGTTATGGGTACTCTCTTACTGTT	1305	
429	LysIleGluPhePro-----IleLeuGluAspSer	438	
1306	AGGTCAATACAGGATCGTAGTCCCTGTTACGGTACCAGTGGTGTGACAGAGACAC	1365	
439	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSer	458	
1366	GAAGAGGCACATCAGCTGCTTAT-----1389		
459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478	
1390	CTTGTGTTCTCCCAAGCAGAGCTTTGCCACCTTGAGCCCATGTCTCATGAATACCC	1449	
479	ValGlySer-----ProPheGluLeuValValSerGlyAsnLys-----Arg	492	
1450	TGTGGCCATCTCAGACAGTCCAGGCACATTATTTCTGAATGGAGCACCCTCTGGG	1509	
493	LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly	510	
1510	CTGAAGAGCTCTCTCTTCTATTATCTGATATGCAAGGAGGAGCATTTGCCAAGCTGG	1569	
511	-----LysGlnAsnSerThr-----MetPheSerLeuThr	520	
1570	ACTCATGCTGCTGTGAAGCAGAGACATGAGGGCCATTTTCCATCTCATCCCT	1629	
521	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspGly	540	
1630	GTGAAGTCAGACATTCCTCTGCTCGCTCGTGTCTCATCTATGCTGCTTTTACCTACCGG	1689	
541	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys	560	
1690	GACGTGATGGGATCTGCAAAATATGATTTGAAAATGCTCTGGCCCAACAGGTGAT	1749	
561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580	
1750	TTGAGCTTCAGCCCATCACAAGTCTCCAGCCTCACAGCCCACTGCGAGTCACAGCG	1809	
581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMet---	599	
1810	GCT---CCTCAGCTGCTGCGCCCTCGTCTGTGGACCAAGCGTCTCTCATGAAG	1866	
600	-----AsnAlaSer-----602		
1867	CCTGATGCTGAGCTCTCGGCTCTCGGTTTACACCTGTCTACAGAAAAGGACCTCACT	1926	
603	-----AsnAspIleThrMetGluAsnValValHisGluLeuGluLeu	616	
1927	GGCTTCCCTGGGCTTTTGAATGACAGACAAATGAAGACTGCATCAATCGTCAATATGTC	1986	

Qy 617 TyAsnThrGlyTyr---TyrLeuGlyMetPheMetAsnSer-----PheAla 631  
Db 1987 TATATTAAATGAATACATATATCTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 2046  
Qy 632 ValPheGlnCysGlyLeuThrValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651  
Db 2047 TTCTAGAGACATGGGCTTTAAAGGCATTCACCAACTCAAAAGATTGCTAAACCCAAATG 2106  
Qy 652 AspGlyValTyrAspAsnAlaGlu-----Tyr 660  
Db 2107 TGTCACAGCTTCAACAGTATGAAATGCATGGACCTGAGGCTACGTGTAGGTTTAT 2166  
Qy 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680  
Db 2167 GAGTCAGATTGAATGGGAAGAGCCATGCACGCCGTGTGTGATCTTGAAGAG----- 2217  
Qy 681 GlySerSerProHis-----ValArgLysHisPheProGluThrTrpIleTrpLeu 697  
Db 2218 -----CCTCACAGGAGACCGTACGAAAGTACTTCCCTGAGACATGGATCTGGAT 2268  
Qy 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717  
Db 2269 TTGGTGGTGAATAACTCAGCAGGTGTGGCTGAGTAGGAGTAAACAGTCCCTGCACACCATC 2328  
Qy 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737  
Db 2329 ACCGAGTGAAGCAGGGGCTTCTCGCTGTCTGGAAGATGCTGGACTTGGTATCTCTCC 2388  
Qy 738 ThrProValGluLeuGlnAlaPheGlnProPheIlePheLeuAsnLeuProTyrSer 757  
Db 2389 ACT---GCCCTCTCCGAGCTTCCAGCCCTTCTTTGTGGAGCTCACAATGCCCTACTCT 2445  
Qy 758 ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777  
Db 2446 GTGATTCTGTGGAGAGGCTTTCACACTCAAGCCACCGCTCTTAAACTACCTTCCCAATGC 2505  
Qy 778 ThrGluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797  
Db 2506 ATCCGGTCTAGTGTCAGCTGGAGGCTCTCCCGCTTCTAGCTGTCCAGTGGAGAG 2565  
Qy 798 Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812  
Db 2566 GAACAAGCGCTCAGTCACTCTGTGCAACCGCGCGCAA----- 2604  
Qy 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832  
Db 2605 -----ACTGTGTCTCGGCGAGTAAACCCCAAGTCAATAGGAATGTGAATTC 2652  
Qy 833 ThrValThrAlaLeuSer-----ProThrAla 841  
Db 2653 ACTGTAGCGCAGAGGCACTAGAGTCTCAAGAGCTGTGTGGAGTCAAGTGCCTTCAGTT 2712  
Qy 842 -----SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856  
Db 2713 CCTGAACACGGAAGAAAGACACAGTCAATCAAGCCTCTGTGTGTTGAACCTGAAGGACTA 2772  
Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876  
Db 2773 GAGNAGGAACAACATTCACCTCCTACTTTGTCCATCAGGTGGTGGTTCCT----- 2826  
Qy 877 LeuLysThrLeuSerPheSerProProAsnThrValThrGlySerGluArgValGln 896  
Db 2827 ---GAAGAAATTATCCCTGAAACTGCCACCAATGTGTGAGAGAAATCTGCCGAGCTTCT 2883  
Qy 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916  
Db 2884 GTCTCAGTTTTGGAGACATATTAGGCTTGCCATGCAAGAAACACACAAAATCTTCTCCAG 2943  
Qy 917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936  
Db 2944 ATGCCCTATGGCTGTGGAGAGCAATATGCTCTCTTCTCTCTAACATCTATGTACTG 3003

Qy 937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956  
Db 3004 GATTATCTAAATGAACACACAGCAGCTTACTCCAGAGATCAAGTCCCAAGGCCATTTGGCTAT 3063  
Qy 957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976  
Db 3064 CTCAACACTGTTTACAGAGACAGTGAACACTACAACTACTGATGGCTCTCAGACACC 3123  
Qy 977 PheGly---AsnTyrAspProSer---GlySerThrTrpLeuSerAlaPheValLeuArg 994  
Db 3124 TTTGGGAGCGATATGGCAGGAACACAGGCAACACCTGGCTCAGAGCTTTGTCTGAAG 3183  
Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014  
Db 3184 ACTTTTGGCCAAAGCTCAGCGCTACATCTTATCATGATGAAGCACACATTACCAAGCCCTC 3243  
Qy 1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034  
Db 3244 ATATGGCTCTCCAGAGCGCAGAGGACAAATGGCTGTTTTCAGAGCTCTGGGTCACTGCTC 3303  
Qy 1035 HisSerGlnLeuGlnGlyLysAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054  
Db 3304 AACAAATGCCATAAAGGAGGAGTAGAAGATCAAGTGAACCTCTCCGCTATATACCAATC 3363  
Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074  
Db 3364 GCCCTTCTGGAGATCTCTCTCACAGTCACTCACCTCTTGTCCGCAATGCCCTGTTTTCG 3423  
Qy 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088  
Db 3424 CTGGAGTCAGCTCGAAGACAGACAGCAAGAAGGGAGCCATGCG---AGCCATGTATATACC 3480  
Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107  
Db 3481 AAAGCAGTCTGGGCTATGCTTTTCCCTGGCAGTAAACAGACAGAGAGAGGAAGTA 3540  
Qy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyMetGlnPheTrp----- 1124  
Db 3541 CTCAAGTCACTTAATAGGAAGCTGTGAAGAAAGACAACCTCTGTCCATTGGGAGCGCCT 3600  
Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle 1142  
Db 3601 CAGAAACCAAGGACACAGTGGGGCATTTTACGAACCCAGCGCTCCTCTGTGAGGTG 3660  
Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer 1159  
Db 3661 GAGATGACATCTATGCTCTCTCGCT---TATCTCAGCGCCAGCCAGCCGCCAACCTCG 3717  
Qy 1160 GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175  
Db 3718 GAGGACCTGACCTCTGCAACCAACATCGTAAGTGGATACGAGAGCAGAGAATGCCAG 3777  
Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195  
Db 3778 GCGGTTTCTCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTCTGCCAATATGGA 3837  
Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215  
Db 3838 GCAGCCACATTTACC---AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3894  
Qy 1216 SerProLeuAlaValValGln----- 1222  
Db 3895 ACATTTCCAGCAAAATCCCAAGTGGACACAAACCCGCTGTACTGTCAGCAGGCTCTCA 3954  
Qy 1223 -----PrometAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238  
Db 3955 TTGCCAGAGCTGCTGGGGAATACAGCATGAAAGTGAAGAGGAAGATGTGTCTACCTC 4014  
Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258  
Db 4015 CAGACATCTCTTGAATACAAATATT-----CTC 4041  
Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275





Db 3125 TTGGGAGCGATATGCGAGGACACAGGCGCAACACCTGGCTCACAGCCTTTGTTCTGAAG 3184  
Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014  
Db 3185 ACTTTTCCCAAGCTCGAGCTCATCTTCCATGATGAGACACACATTACCAGCCCTC 3244  
Qy 1015 ThrTriLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034  
Db 3245 ATATGGCTCTCCAGAGCGCAGAGGACAATGGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3304  
Qy 1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054  
Db 3305 AACAAATGCCATAAAGGAGAGTAGAAGATGAATGACCTCTCCGCTTATATCACCATC 3364  
Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGlnSerIleHisPhe 1074  
Db 3365 GCCCTCTGGAGATTCCTCTCACAGTCACCTCACCTGTTGTCGCAATGCCCTGTTTGC 3424  
Qy 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088  
Db 3425 CTGGAGTCAGCCTGGAAGACAGACAGACAGAGAGGGGACCATGCG---AGCCATGTATATACG 3481  
Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107  
Db 3482 AAGCACTGTGGCTATGCTTTGCTGCGAGTGAACAGGACAGAGGAGGAAGTA 3541  
Qy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp----- 1124  
Db 3542 CTCAAAGTCACTTAATGAGGAAGCTGTGAAGAAAGACAACTCTCTCCATTGGGAGCGCCT 3601  
Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle 1142  
Db 3602 CAGAAACCCAGGACAGGAGGGGCACTTTTACGAACCCAGGCTCCCTCTGTGAGGTG 3661  
Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer 1159  
Db 3662 GAGATGACATCCCTATGTCTCTCGCT---TATCTCAGGCCCCAGCCGCCCAACTCG 3718  
Qy 1160 GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175  
Db 3719 GAGGACCTGACCTCTGCAACCAACATCGTGAAGTGGATCAGGAGCAGCAATGCCCCAG 3778  
Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195  
Db 3779 GCGGTTTCTCCACCCAGGACACAGTGTGGCTCTCATGCTCTGTCCAAATATGGA 3838  
Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215  
Db 3839 GCGCCACATTAC---AGGACTGGGAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3895  
Qy 1216 SerProLeuAlaValValGln----- 1222  
Db 3896 ACATTTTCCAGCAAAATCCCAAGTGGACAAACAATGCGCTGTACTGCGAGCGTCTCA 3955  
Qy 1223 -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238  
Db 3956 TTGCCAGAGCTGCTCGGGGAATACAGCATGAAGTGACAGAGAGGATGTGTCTACCTC 4015  
Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258  
Db 4016 CAGACCTCTCTGAAATACAATATT-----CTC 4042  
Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275  
Db 4043 CCAGAAAGGAAGAGTTCCCTTTGCTTTAGGAGTGCAGACTCTGCTCCTCAACTGTGTAT 4102  
Qy 1276 AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly----- 1292  
Db 4103 GAACCCAAAGCCACACACAGCTTCCAAATCTCCCTAAGTGTCTAGTTACACAGGAGCGCG 4162  
Qy 1293 ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311

Db 4163 TCTGCTCCAAACATGGCGATGCTTGAATGAGTGGTCTCTGGCTTCATTCCCTGAAG 4222  
Qy 1312 GluAlaIleSerLeu-----SerGluThrValLysValGluTyrAspHisGly 1328  
Db 4223 CCAACAGTGAATACTTGAAGAATCTAACCATGTGACCGGACAGAACTCAGCAGCAAC 4282  
Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGlnThrGlnPheCysValAsnIleProAla 1348  
Db 4283 CATGTCTTGAATTAACCTTGAATAAGGTGTCAAATCAGACACTGAGCTTCTTCTCAGGTT 4342  
Qy 1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368  
Db 4343 CTGCAAGATGTCCTCAGTAAGATCTCAACAGCAGCATAGTGAAGTCTATGATTACTAC 4402  
Qy 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380  
Db 4403 GAGACGGATGAGTTTGCAATCGCTGAGTACAATGCT 4438  
RESULT 13  
US-10-116-802-21  
; Sequence 21, Application US/10116802  
; Publication No. US20030065157A1  
; GENERAL INFORMATION:  
; APPLICANT: Amy Lasek  
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER  
; FILE REFERENCE: PA-0045 US  
; CURRENT APPLICATION NUMBER: US/10/116,802  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 60/281,593  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 519  
; SOFTWARE: PERL Program  
; SEQ ID NO 21  
; LENGTH: 4769  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 273154CB1  
US-10-116-802-21  
Alignment Scores:  
Pred. No.: Length: 4769  
Score: 1441.00 Matches: 451  
Percent Similarity: 46.20% Conservative: 266  
Best Local Similarity: 29.08% Mismatches: 551  
Query Match: 19.61% Indels: 284  
DB: 13 Gaps: 59  
US-10-020-095-4 (1-1428) x US-10-116-802-21 (1-4769)  
Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31  
Db 279 CTCCTTGGTCTCTCCGCCACAGACGCTCTGGAACACCGCAGTATATGTTCTG 338  
Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuGluHis 51  
Db 339 GTCCCTCCCTGCTCCACACT---GAGACCACTGAGAGGGCTGTGCTCTTCTGAGTAC 395  
Qy 52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuVal 71  
Db 396 CTGAATGAGACACTGACTGTAAAGTCTTCTTGGAGTCTGTCAGGGGAAACAGGAGCCTC 455  
Qy 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89  
Db 456 TTCATGTACCTGGAGCGGAGAAATGACGTACTCCACTGTGTCGCTTC----- 503  
Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106  
Db 504 -----GCTGTCCCAAGCTTCAATCAATGAGGAGGTAATGTTCTCTCACTGTCACAGTG 557  
Qy 107 ThrGlyArgThrGlnAspGluLeuPheSerAsnSerThrArgLeuSerPheLeuThr 126

Db	558	AAAGGACCAACCCCAAGAA-----TTTAAAGAAGCGGACCA	CAGTGTATGGTTAAGAAC	608
Qy	127	LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal	146	
Db	609	GAGCACAGCTCTGGTCTTTGTCCAGACAGACAAATCAATCTACAAAC	CAGGCGACACAGTGTG	668
Qy	147	LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle	166	
Db	669	AAATTTCCGTGTGTCTCCATGGATGAAACACTTCCACCCCTGGAATGAGTTGATCCCACTA	728	
Qy	167	Leu---IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp	185	
Db	729	GTATACATTCAGGATCCCAAGGAAATCGCATCGCAATGGCAGAGTTTCCAGTTAGAG	788	
Qy	186	LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer	205	
Db	789	GGTGGCCTCAAGCAATTTTCTTTCCCTCTCATCAGAGCCCTTCCAGGCGCTCTACCAAG	848	
Qy	206	IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu	223	
Db	849	GTGGTGTACAGAAGAAATCAGGTGGAGGACAGACAC-----CCTTTACCGTGGAGAA	905	
Qy	224	TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer	243	
Db	906	TTTCTTCTCCAAAGTTTGAAGTACAAGTAACAGTGCACAAAGATAATCA	CCTATCTTGAA	965
Qy	244	LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp	263	
Db	966	GAGAGATGAATGTATCAGTGTGGCCTATACACATATGGAAAGCTGTCCCTGGACAT	1025	
Qy	264	ValThrLeuThrPheLeuProLeu-----	271	
Db	1026	GTGACTGTGAGCAITTCAGAAAGTATAGTCACGCTTCCGACTGCCACGGTGAAGATTCA	1085	
Qy	272	-----	SerPheTrpGlyLys	276
Db	1086	CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGCTCTCTATCAGCAA	1145	
Qy	277	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp	296	
Db	1146	GTAAAA-----ACCAAGTCTTCCAGCTGAAGAG-----AAGAG	1181	
Qy	297	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	316	
Db	1182	TATGAAATGAAA-----CTTCACACTGAGGCCAGATCAAA	1217	
Qy	317	SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal	331	
Db	1218	GAAGAAGAACAGTGGTGGAAATTCAGTGAAGGAGGCTCCAGTGAATATCACAAAGACCAAT	1277	
Qy	332	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle	351	
Db	1278	ACCAAACTCTCA-----TTTGTGAAAGTGGACTCACACITTCGACAGGGA-----ATT	1325	
Qy	352	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	371	
Db	1326	CCCTTCTTTGGG-----	CAG	1340
Qy	372	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsnValValIle	391	
Db	1341	GTGGCCCTAGTAGTGGAAAGGCGTCCCTATACCA-----AATAAGTCA	1388	
Qy	392	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	411	
Db	1389	TTTCATC---AGAGGAAATGAAGCAAACTATTAC-----TCCAATGCTACCCAGGTAG	1439	
Qy	412	MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe	428	
Db	1440	CATGGCCTTGTACAGTCTCTATACACACCAACCAATGTTATGGTACTCTCTTACTGTT	1499	
Qy	429	LysIleGluPhePro-----IleLeuGluAspSer	438	
Db	1500	AGGCTCAATTAACAGGATCGTAGTCCCTGTTATACGGCTACCAAGTGGGTGCAGAGAACAC	1559	

Qy	439	SerGlnLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer	458
Db	1560	GAAGAGGCACATCACATCGCTTAT	1583
Qy	459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAenIleLys	478
Db	1584	CTTGTGTTCTCCCAAGCAAGAGCTTTGTCCACCTTGGAGCCCATGTCTCATGAACACCC	1643
Qy	479	ValGlySer	492
Db	1644	TGTGGCCATCTACAGACGTCGAGGCACATATATTCTGAATGGAGGCACCCCTGTGGGG	1703
Qy	493	LeuLysGlnLeuSer	510
Db	1704	CTGAAGAAGCTCTCTTCTATTATCTGATAATGGCAAGGAGGACCATTTGCCGAAGCTGGG	1763
Qy	511		520
Db	1764	ACTCATGAGTGTGTGAAGACGAGGAGACATGAAGGCCCATTTTCCATCTCAATCCCT	1823
Qy	521	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly	540
Db	1824	GTGAAGTCACAGATTGCTCTCTGTCGCTCGGTGTGTCATCTATGCTGTTTACCTACCGGG	1883
Qy	541	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysLys	560
Db	1884	GACGTGATTGGGATCTCGAAATATGATGTTGAAATTTGTCGGCCACAAGATGGAT	1943
Qy	561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580
Db	1944	TTGAGCTTCAGGCCATCACAAAGTCTCCAGCCTCACAGCCACCTCGGAGTCACAGCG	2003
Qy	581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	600
Db	2004	GCT---CCTCAGTCGGCTCGGCCCTCGGCTGTGACCAAGACGCTGCTCATGAAG	2060
Qy	601	AlaSerAsnAspIleThrMetGluAsnValValHisGlnLeu---GluLeuTyrAsnThr	619
Db	2061	CCTGATGCTGAGCTCTCGGCGTCTCTGCTTTACAACCTGCTACAGAAAAGGACCTCACT	2120
Qy	620	GlyTyr---	625
Db	2121	GGCTTCCCTGGGCTTTGAATGACACGAGCGATGAAGACTGCATCAATCGTCATATGCT	2180
Qy	626	PheMetAsnSer---	631
Db	2181	TATATTAAATGAATACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC	2240
Qy	632	ValPheGlnGlyCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle	651
Db	2241	TTCTAGAGACATGGCGCTTAAGGCAATCCACCACTCAAGAATTTGTAAACCCCAATG	2300
Qy	652	AspGlyValTyrAspAsnAlaGlu---	660
Db	2301	TGTCACAGCTTCAACACAGTATGAAATGCATGGACCTGAAGCTCTAGCTGTAGGTTTTAT	2360
Qy	661	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	680
Db	2361	GAGTCAGATGTAATGGGAAGAGGCCATGACGCGCTGTGTGATGTTGAAGAG---	2411
Qy	681	GlySerSerProHis---	697
Db	2412	-----CCTCACACGGAGACCGTACGAAAGTACTTCCTCAGACATGGATCTGGAT	2462
Qy	698	AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle	717
Db	2463	TTGTGTGTGTTAACTCAGCAGAGTGTGGCTGAGGTAGGATTAACAGTCCCTGACCAATC	2522
Qy	718	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuThrThr	737
Db	2523	ACCGAGTGAAGCAGCGGGCTCTCGCTGCTCTCAAGATGCTCGATCTGGATCTCTCTCC	2582

738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757  
2583 ACT---GCCCTCTCCGAGGCTTCCAGCCCTCTTTGTGGAGTGCACAAATGCTTACTCT 2639  
758 ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777  
2640 GTGATTCTGTGAGAGGCTTCACTCAAGCCACGGTCTCTAACTACCTTCCCAATGC 2699  
778 ThrGluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797  
2700 ATCCGGTCTAGTGTGCAGCTGGAAGCCTCTCCGCCCTCTAGCTGTCCAGTGGAGAAG 2759  
798 Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuValProSer 812  
2760 GAACAAGCGCTCACTCATCTGTGCAACGGCGGCAGAA----- 2798  
813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832  
2799 -----ACTGTGTCCTGGCAGTAACCCCAAAGTCATTAGGAATGTGAATTC 2846  
833 ThrValThrAlaLeuSer-----ProThrAla 841  
2847 ACTGTGAGCGAGGACACTAGAGTCTCAAGAGCTGTGTGGACTGAGGTGCCTTCAGTT 2906  
842 -----SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856  
2907 CCTGAACACGAAGAAAGACACAGTCATCAAGCCTCTGTGTGTAACCTGAAGACTA 2966  
857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876  
2967 GAGAAGAAACAAACATTCAACTCCCTACTTTGTCCATCAGTGTGTAGGTTCT----- 3020  
877 LeuLysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln 896  
3021 ---GAAGAAATATCCCTGAAACTCCACACAAATGTGTAGAGAACTGCCGAGCTTCT 3077  
897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916  
3078 GTCTCAGTTTGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCAG 3137  
917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936  
3138 ATGCCCTATGGCTGTGGAGAGCAAAATGTGCTCTTTGCTCTACACTATGTACTGT 3197  
937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956  
3198 GATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGGCCATTGGCTAT 3257  
957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976  
3258 CTCACACTGGTTACCGAGACAGCTTGAACCTACAAACACTATGATGCTCTCTACAGACC 3317  
977 PheGly--AsnTyrAspProSer--GlySerThrTrpLeuSerAlaPheValLeuArg 994  
3318 TTGGGGAGCGATATGGCAGGAACCGGGCAACCTGGTCTCAGGCTTTGTTCGAAG 3377  
995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014  
3378 ACTTTTGCCCAAGCTCGAGCCTACATCTTCATCGATGAAGCACACATACCCAGCCCTC 3437  
1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034  
3438 ATATGGCTCTCCAGAGCGAAGACATGGCTGTTTCAGGAGCTCTGGTCACTGCTC 3497  
1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054  
3498 AACAAATGCCATAAAGGGAGGAGTAGAAGATGAAGTGAACCTCTCCGCTATATCACCATC 3557  
1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074  
3558 GCCCTTTTGGAGATTCCTCTCACAGTCACTCACCTGTGTCCCAATGGCTCTTTTTCG 3617  
1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088

Db	3618	CTGAGATCGACCCCTGGAGACAGCAGCAAGAAGGGACCATTGGC---AGCCATGTATATATACC	3674
Qy	1089	LeuAlaLeuIleThrTyRAlaLeuSerSerValGlySer---ProLysAlaLysGluAla	1107
Db	3675	AAAGCACTGTCGCCATATGCTTTTGCCCTGGCAGGTAAACCAGGACAAGAGGAAGTA	3734
Qy	1108	LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp-----	1124
Db	3735	CTCAAGTCATCTAATGAGGAAGCTGTGAAGAAACAACACTCTCTCCATTCGGAGCCCT	3794
Qy	1125	ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle	1142
Db	3795	CAGNAACCCAGGCACAGTGGGCATTTTACGACCCAGCTCCCTCTGCTGAGGTG	3854
Qy	1143	GluValAlaAlaTyRAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer	1159
Db	3855	GAGATGATCATCTATGTCTCTCGT---TATCTCAGCGCCAGCAGCCCAACCTCG	3911
Qy	1160	GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnAArgAsnSerLeu	1175
Db	3912	GAGGACCTGACCTCTGCACCAACATCGTGAAGTGATCAGGAAGCAGAGATGCCAG	3971
Qy	1176	GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla	1195
Db	3972	GGCGGTTTCCTCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTGTGCCAATATGGA	4031
Qy	1196	AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro	1215
Db	4032	GCAGCCACATTACC---AGGACTGGGAAGCTGCACAGGTGACTATCCAGTCTTCAGGG	4088
Qy	1216	SerProLeuAlaValValGln-----	1222
Db	4089	ACATTTCCTCAGCAAAATCCCAAGTGGACAACAACACCGCTGTTACTGTCAGCAGGTCTCA	4148
Qy	1223	-----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys	1238
Db	4149	TTCGACAGCTGCCCTGGGGAAATCAGCATGAAGTGCAGGAGAGATGTGTCTACCTC	4208
Qy	1239	GlnLeuAsnValValTyRAsnValLysAlaSerGlySerArgArgArgSerIle	1258
Db	4209	CAGACATCCTTGAATACATAATT-----CTC	4235
Qy	1259	GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp	1275
Db	4236	CCAGAAAGGAAGAGTTCCCTTGTCTTAGGAGTGCAGACTGTGCTCAAACTTGTGAT	4295
Qy	1276	AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly-----	1292
Db	4296	GAACCCAAAGCCACACACCAGCTCCAAATCTCCCTAAGTGTAGTACAGGAGCGCG	4355
Qy	1293	---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer	1311
Db	4356	TCTGCCCTCCAAACATGGCGATCGTTGTATGTGAAGATGGTCTCTGGCTTCATTCOCCTGAAG	4415
Qy	1312	GluAlaIleSerLeu-----SerGluThrValLysLysValGluTyRAspHisGly	1328
Db	4416	CCAACGTGAAATGCTTGAAGATCTAACCATGTGAGCCGGACAGAGTCAGCAGCAAC	4475
Qy	1329	LysLeuAsnIleTyRLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla	1348
Db	4476	CATGCTCTGTATTACCTTGTAAAGGTGTCAAAATCAGACTGAGCTTGTCTTCACGGTT	4535
Qy	1349	ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyR	1368
Db	4536	CTGCAAGATGCCAGTAAGAGATCTGAACACCAGCCATAGTGAAGAGTCTATGATTACTAC	4595
Qy	1369	GluProArgGlnAlaValArgSerTyRAsnSer	1380
Db	4596	CAGACGGATGAGTTTGCAAATTGTGTGAGTACAATGCT	4631





Qy	521	ProGluAsnSerTrpThrProLysAlaCysValileValTyrTyrIleGluAAspAspGly	540
Db	1588	GTGAAGTCACAGCATGTCTCTCGCTCGGTGTCTCATCTATGTGTGTGTACCTACCGGG	1647
Qy	541	GlurIleIleSerAspValLeuValIleProValGlnLeuValPheLysAsnLysIleLys	560
Db	1648	GACGTGATGGGGATTCGCAAAATATGATGTTGAAAATTGTCGCGCCACAAGTGGAAT	1707
Qy	561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580
Db	1708	TTGAGCTTCAGCCCATCAAAAGTCTCCAGCCCTCACAGCCCACTGCGAGTCACAGCG	1767
Qy	581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	600
Db	1768	GCT---CCTCAGTCCGTCGCGCCCTCGGCTGTGGACCAAGCGTGCCTCATGAAG	1824
Qy	601	AlaSerAsnAspIleThrMetGluAsnValValHisGluLeu---GluLeuTyrAsnThr	619
Db	1825	CCTGATGCTGAGCTCTCGGCGCTCTCGGTTTACACCTGTACAGAAAGGACCTCACT	1884
Qy	620	GlyTyr-----TyrLeuGlyMet	625
Db	1885	GGCTTCCTCGGCGCTTTGAATGACAGGACGATGAGACTGCATCAATCGTCATAATGTC	1944
Qy	626	PheMetAsnSer-----PheAla	631
Db	1945	TATATTATGGAATCACATATATCTCCAGTATCAAGTACAATGAAAGGATATGTACAGC	2004
Qy	632	ValPheGlnGlyCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle	651
Db	2005	TTCTAGGACATCGGGCTTAAGGCATTACCAACTCAAAGATTCTGTAACCCAAAATG	2064
Qy	652	AspGlyValTyrAspAsnAlaGlu-----Tyr	660
Db	2065	TGTCACAGCTTCAACAGTATGAATAATGATGGACCTGAAGTCTAGGTGTAGTTTTAT	2124
Qy	661	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	680
Db	2125	GAGTCAGATGTAATGGGAAGAGGCCATGTCACGCCTGTGTCATGTTGAAGAG-----	2175
Qy	681	GlySerSerProHis-----ValArgLysHisPheProGluThrTrpIleTrpLeu	697
Db	2176	-----CCTCACAGGACCGTACGAAAGTACTTCCCTGAGACATGGATCTGGAT	2226
Qy	698	AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle	717
Db	2227	TTGTGTGGTGAATACTCAGCAGGGGTGGCTGAGGTAGGAGTAAACAGTCCCTGCACCATC	2286
Qy	718	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	737
Db	2287	ACCGAGTGAAGGCGAGGGCCCTCTGCTGCTCAAGATGTGACATGTGTTATCTCTCC	2346
Qy	738	ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer	757
Db	2347	ACT---GCCTCTCTCCGAGCCCTCCAGCCCTCTTTGTGGAGCTTACAAAGCCTTACTCT	2403
Qy	758	ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla	777
Db	2404	GTGATTCGTGGAGAGCCCTTCACACTCAAGCCACGGTCCCTAAACTACCTTCCCAATGC	2463
Qy	778	ThrGluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer	797
Db	2464	ATCCGGGTTCAGTGTGCAGCTCGAAGCCCTCTCCGCCCTCTCTGTGTCGCCAGTGGAGAG	2523
Qy	798	Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	812
Db	2524	GAAACAAGCCCTCACTGCATCTGTGCAAAACGGGGCGCAA-----	2562
Qy	813	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle	832
Db	2563	-----ACTGTCTCTGGCGAGTAAACCCCAAGTCATTAGGAATGTGAATTC	2610

Qy	833	ThrValThrAlaLeuSer-	-----ProThrAla	841
		:    :	:    :	
Db	2611	ACTGTGAGCGCAGAGCAGCTAGAGTCTCAAGAGCTGTGTGGAGCTGAGGTGCCTTCAGTT	2670	
Qy	842	-----SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle	856	
Db	2671	CCTGAACACGGAAGAAAGACACAGTCATCAAGCCTCTGTTGGTGAACCTGAAGGACTA	2730	
Qy	857	GluIysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr	876	
		:    :	:    :	
Db	2731	GAGAAGAAACAAACATTCACACTCCCTACTTGTCCATCAGGTGGTGAAGTTCT-	2784	
Qy	877	LeuIysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln	896	
		:    :	:    :	
Db	2785	---GAAGAAATATCCCTGAACCTCCACCAAAATGTGGTAGAAGATCTGCCGAGCTTCT	2841	
Qy	897	IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg	916	
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Db	2842	GTCTCAGTTTGGGAGACATATTAGGCTCTGCATGCAAAACACACAAAAATCTTCCAG	2901	
Qy	917	MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu	936	
		:    :	:    :	
Db	2902	ATGCCCTATGCTGTGGAGAGCAATATGGTCTCTTCTCTCTCAACATCTATGACTG	2961	
Qy	937	AspTyrLeuThrLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe	956	
		:    :	:    :	
Db	2962	GATTATCTAAATGAACACACAGCAGCTTACTCCAGAGGTCAAGTCCAAGGCCATTGGCTAT	3021	
Qy	957	MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla	976	
		:    :	:    :	
Db	3022	CTCAACACTGGTTACCAAGACAGACTGAATACAAACACTATGATGCTCTCTCAGACACC	3081	
Qy	977	PheGly---AsnTyrAspProSer---GlySerThrTyrLeuSerAlaPheValLeuArg	994	
		:    :	:    :	
Db	3082	TTTGGGAGCGATATGGCAGAAACACAGGCCGCAACACCTGGCTCAGACCTTTGTTCTGAAG	3141	
Qy	995	CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr	1014	
		:    :	:    :	
Db	3142	ACTTTTGCCCAAGCTCAGAGCTACATCTTCATCGATGAAGCACATATCCCAAGCCCTC	3201	
Qy	1015	ThrTyrLeuLysGlyHisGlnLysSerAsnGlyGluPheTyrAspProGlyArgValIle	1034	
		:    :	:    :	
Db	3202	ATATGGCTCTCCAGAGCAGAGGACATGGCTGTTTCAGGAGCTCTGGGTACTGCTCT	3261	
Qy	1035	HisSerGluLeuGlnGlyIleAsnLysSerProValThrLeuThrAlaTyrIleValThr	1054	
		:    :	:    :	
Db	3262	AACAATGCCATAAAGGAGGAGTAGAAGATGAAGTACCTCTCCGCTATATCACCATC	3321	
Qy	1055	SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe	1074	
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[illegible]

## RESULT, T 15

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US-09-750-972-4
; Sequence 4, Application US/09750972
; Publication No. US20040072993A1
; GENERAL INFORMATION:
; APPLICANT: Pramod K. Srivastava
; TITLE OF INVENTION: ALPHA(2) MACROGLOBULIN RECEPTOR AS A HEAT SHOCK
; TITLE OF INVENTION: PROTEIN RECEPTOR AND USES THEREOF
; FILE REFERENCE: 8449-134
; CURRENT APPLICATION NUMBER: US/09/750,972
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/750,972
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/668,724
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 4422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-972-4

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QY 332 ThrGlyLeuSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351  
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Job time : 1752 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 18, 2004, 00:38:25 ; Search time 214 seconds

(without alignments)

3703.130 Million cell updates/sec

Title: US-10-020-095-4

Perfect score: 7348

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4535.5	61.7	3033	US-09-833-381-1810	Sequence 1810, Ap
2	1441	19.6	4577	US-09-241-606-1	Sequence 1, Appl
3	1412	19.2	4792	US-09-566-921-109	Sequence 109, App
4	1346.5	18.3	4079	US-09-016-434-1174	Sequence 1174, Ap
5	973.5	13.2	5211	US-08-447-411-1	Sequence 1, Appl
6	931	12.7	5056	US-08-793-126-2	Sequence 2, Appl
7	931	12.7	5056	US-09-132-271-2	Sequence 2, Appl
8	931	12.7	5067	US-09-142-334-23	Sequence 23, Appl
9	930	12.7	5129	US-09-566-921-107	Sequence 107, App
10	894	12.2	5948	US-08-662-227-1	Sequence 1, Appl
11	894	12.2	5948	US-09-017-947-1	Sequence 1, Appl
12	894	12.2	5948	US-09-925-442-1	Sequence 1, Appl

13	885	12.0	5924	1	US-08-447-411-44	Sequence 44, Appl
14	768.5	10.5	4138	1	US-08-447-411-75	Sequence 75, Appl
15	768.5	10.5	4138	2	US-08-662-227-33	Sequence 33, Appl
16	768.5	10.5	4138	4	US-08-662-227-33	Sequence 33, Appl
17	768.5	10.5	4138	4	US-09-925-442-33	Sequence 33, Appl
18	272.5	3.7	5004	4	US-09-489-039A-4453	Sequence 4453, Ap
19	245	3.3	18431	4	US-09-221-017B-1090	Sequence 1090, Ap
20	234	3.2	339	4	US-09-311-352B-1	Sequence 1, Appl
21	215.5	2.9	750	4	US-09-241-606-3	Sequence 3, Appl
22	211.5	2.9	5151	4	US-09-543-681A-3437	Sequence 3437, Ap
23	203.5	2.8	14066	4	US-09-601-188-56	Sequence 56, Appl
24	185	2.5	549	4	US-09-311-352B-3	Sequence 3, Appl
25	185	2.5	7158	4	US-09-543-681A-2132	Sequence 2132, Ap
26	180	2.4	4026	4	US-09-252-991A-10214	Sequence 10214, A
27	177.5	2.4	8334	4	US-09-543-681A-1952	Sequence 1952, Ap
28	174.5	2.4	7101	1	US-08-480-604A-9	Sequence 9, Appl
29	174.5	2.4	7101	2	US-08-405-496A-9	Sequence 9, Appl
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34	171	2.3	9873	4	US-09-328-352-1360	Sequence 1360, Ap
35	165.5	2.3	7577	4	US-09-637-048C-3	Sequence 3, Appl
36	165.5	2.3	7621	4	US-09-637-048C-6	Sequence 6, Appl
37	165	2.2	6114	4	US-09-543-681A-1366	Sequence 1366, Ap
38	165	2.2	28473	4	US-08-961-527-83	Sequence 83, Appl
39	164.5	2.2	4977	4	US-09-071-035-257	Sequence 257, App
40	164.5	2.2	4977	4	US-09-071-035-261	Sequence 261, App
41	164.5	2.2	4977	4	US-09-071-035-265	Sequence 265, App
42	164.5	2.2	13993	4	US-09-220-132-20	Sequence 20, Appl
43	163.5	2.2	13930	4	US-09-976-594-1011	Sequence 1011, Ap
44	163.5	2.2	14070	4	US-09-108-006C-2	Sequence 2, Appl
45	163	2.2	37948	3	US-09-251-645-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-833-381-1810  
; Sequence 1810, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1810  
; LENGTH: 3033  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-833-381-1810

Alignment Scores:  
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Best Local Similarity: 97.78% Mismatches: 1  
Query Match: 61.72% Indels: 17  
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US-10-020-095-4 (1-1428) x US-09-833-381-1810 (1-3033)

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Qy  
306 CTCACGAAGATTATATGATGTTGTTTATGACATGACAGATATGCTGAGAGTTTATG 365  
Db  
666 GluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGlySerProHis 685  
Qy  
366 GAGGAAATGAAGACATATTGTAGATATTCTATGACTTTCTTTGGGTAGCATCCACAT 425  
Db  
586 ValArgLysHisPheProGluThrTripletLeuAspThrAsnMetGlyTyrArgIle 705  
Qy  
426 GTCCGAAGCAATTTTCCAGAGACTGATGATTTGGCTAGACCAACATGCGGTACAGATT 485  
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706 TyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPhe 725  
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486 TACCAAGATTTGAAGTAACGTACCTGATTCTATCACTCTTTGGGTGGCTACTGTTTT 545  
Db  
726 ValIleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPhe 745  
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546 GTGATCTCTGAGGACCTGGGTCTTGGACTAACCACTACTCCAGTGGAGTCCAAAGCCTTC 605  
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746 GlnProPhePheLeuPheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAla 765  
Qy  
506 CAACATTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGAGGTGAAGATTGCT 665  
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766 LeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu 785  
Qy  
666 TTGAAATAACTATATTCAATTTATTGAAAGATGCCACTGAGGTTAAGGTAATCAATTGAG 725  
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806 GlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProThr 825  
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786 CAGACCCCTCTGTTTCCAGTGAGGATGGGGCAACTGTTCTTTTCCCATCAGGCCAACA 845  
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Qy  
846 CATCTGGAGAAATTCCTATCAGAGTCACAGCTCTTTCCACCCACTGCTCTGATGCTATC 905  
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846 ThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeu 865  
Qy  
906 ACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATATTCACAATCCATCTTA 965  
Db  
866 LeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhePro 885  
Qy  
966 TTAGACTTGATGACATAGCTGACAGAGTTCAGATCACTGCAATTGGAGATGTTCTTGT 1025  
Db  
886 ProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeuGly 905  
Qy  
1026 CCTAATACAGTACTGTCAGCTGGAAGAGTTCAGATCACTGCAATTGGAGATGTTCTTGT 1085  
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906 ProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsn 925  
Qy  
1086 CATTCCATCAATGGCTTAGCTCTATTGATTCGGATGCTTTATGGCTGTGTGTGAACAGAAC 1145  
Db  
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Qy  
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1326 ACTTGTTGTGAGCTTTTGTTTTAAAGATGTTCTTGAAGCCGATCTTACATAGATATT 1385  
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1006 AspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGlnLysSerAsnGly 1025  
Qy  
1386 GATCAGAATGTGTTTACACAGAAACATACACTTGGCTTAAAGGACATCAGAAATCCACGGT 1445  
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Qy  
1566 ATTGATGTGCAAGAGTCTATCCATTTTGGAGTCTGAATTCAGTAGGAAATTTTCAGAC 1625  
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1746 TCATCAGAGTCCAAACTTTCTGACTCTCTGGCAGCCAGCTCCCTGGATATTGAAGTTGCA 1805  
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1806 GCCATGCACTGCTCTCACACTTCTTACAATTTTCAGACTTCTGAGGGAATCCCAATATG 1865  
Db  
1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyPheAlaSerThrGlnAspThrThr 1185  
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Db  
1186 ValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnIle 1205  
Qy  
1926 GTGGCTTTAAGGCTCTGCTGAAATTTGCAGCCCTAATGAATACAGAAAGGACAAATATC 1985  
Db  
1206 GlnValThrValThrGlyProSerSerProSerPro----- 1217  
Qy  
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Qy  
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Db

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QY 1289 SerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMet 1308
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QY 1309 ValProSerGluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly 1328
Db 2346 GTGCCCTTCAGAGCAATTTCTCTGAGCGAGACAGTGAAGAAATGAAATATGATCATGGA 2405
QY 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
Db 2406 AAACCTCAACCTCTATTAGATTCTGTAATGAAACCCAGTTTGTGTATATATCTCTGCT 2465
QY 1349 ValArgAsnPhelysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
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QY 1369 GluProArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAsp 1388
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QY 1389 LeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHis 1408
Db 2586 CTTTGCAAGTATGCCAGGCTGCCGTCTTGTGAGATGGAGCTTCAGGCTCCCATCAT 2645
QY 1409 HisSerValIlePheIlePheCysPheLysLeuLeuTyrPheMetGluLeuTyrLeu 1428
Db 2646 CACTCTTCAGTCATTTTATTTCTGTTTCAAGCTTCTGACTTATGAACTTTGGCTG 2705

RESULT 2
US-09-241-606-1
; Sequence 1, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; FILE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.445003
; CURRENT APPLICATION NUMBER: US/09/241,606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (44)..(112)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)..(4468)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (113)..(4468)
US-09-241-606-1

Alignment Scores:
Pred. No.: 4,6e-145 Length: 4577
Score: 1441.00 Matches: 451
Percent Similarity: 46.20% Conservative: 266
Best Local Similarity: 29.06% Mismatches: 551
Query Match: 19.61% Indels: 284
DB: 4 Gaps: 59

US-10-020-095-4 (1-1428) x US-09-241-606-1 (1-4577)
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QY 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51

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Db 203 CTGAATGAGACAGTGTAGTGTCTTCTTGAGTCTGTCAAGGGAACAGGAGCTC 262
QY 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
Db 263 TTCACGTGACCTGGAGCGGAGAGTACGTACTCCACTGTGTCGCTTC--- 310
QY 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
Db 311 -----GCTGCCCAAACTCTTCACCAATGAGAGGTAATGTTCTCCTCACTGTCACAGTG 364
QY 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
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QY 127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146
Db 416 GAGGACAGTCTGGTCTTTGTCAGACAGACAAATCAATCTACAAACCAAGGCGACAGATG 475
QY 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166
Db 476 AATTTTCGTGTGTCCTCATGATGAAACTTTCACCCCTCGAATGATGATTCCTCACTA 535
QY 167 Leu---IleLysAspProLysSerAsnLeuIleGlnGlnThrLeuSerGlnGlnSerAsp 185
Db 536 GTATACATTCAGGATCCCAAGAAATCGCATCGCACAATGCGAGAGTTTCAGTTAG 595
QY 186 LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205
Db 596 GGTGCTCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTCCAGGGTCTCTACAG 655
QY 206 IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu 223
Db 656 GTGTGGTTACAGAAATAATCAGTGGAAAGGACAGAGCAC---CCTTTCCCGTGAGGAA 712
QY 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243
Db 713 TTTGTCTTCCCAAGTTTGAAGTACAGTACAGTGCACAAAGATAATCACCATTGGA 772
QY 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263
Db 773 GAAGAGATGATGATCAGTGTGTCCTATACACATATGGAAGCCTGTCCTGGACAT 832
QY 264 ValThrLeuThrPheLeuProLeu----- 271
Db 833 GTGACTGTGAGCATTTGCAAGAAAGTATAGTACGCTTCCGACTGCCACGTGAAGATTCA 892
QY 272 -----SerPheTyrGlyLys 276
Db 893 CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCA 952
QY 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296
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QY 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
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QY 317 SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal 331
Db 1025 GAAGAAGGAACAGTGTGGAATTTGCTGAAAGGAGTCCAGTGAATAATCACAAGAACCATA 1084
QY 332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351
Db 1085 ACCAAACTCTCA---TTTGTGAAGTGGACTCACACTTCGACAGGGA-----ATT 1132
QY 352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371

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[illegible]

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Db      4283  CATGTCCTGATTACCTTTCATTAAGGTGTCAAAATCAGACACTGAGCTTGTTCCTTCAACGGTT 4342
Qy      1349  ValArgAsnPhelysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
Db      4343  CTCCAAGATGTCACAGTAGAGATCTCAACACGACCATAGTGAAGAGCTATGATTACTAC 4402
Qy      1369  GluProArgGlnAlaValArgSerTyrAsnSer 1390
Db      4403  GAGACGGATGAGTTTCGAATCGCTGAGTACAATGCT 4438

RESULT 3
US-09-566-921-109
; Sequence 109, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debra W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 109
; LENGTH: 4792
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6682888 369213.15
US-09-566-921-109

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Db 671 AAATTCGTGTGTCTCCATGGATGAAACTTTCACCCCTGAAATGATGATTCACCTA 730  
Qy 167 Leu---IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185  
Db 731 GTATACATTCAGATCCCAAGGAAATCGCATCGCAATGGCAGAGATTTCAGTAGAG 790  
Qy 186 LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIle-LeuGlyAspTrpSe 205  
Db 791 GGTGGCTCAAGCAATTTCTTTCCCTCTCATCAGAGCCCTTCCAGGGCTCCTACAA 850  
Qy 205 rIleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGI 223  
Db 851 GGTGGTGGTACAGAGAAATCAGGTGGAGGACAGAGCAC---CCTTTCCACCGTGGAGGA 907  
Qy 223 uTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSe 243  
Db 908 ATTTGTTCTTCCAGTTGAGTACAGTAAAGTCCCAAGATAATCACCATCTTGA 967  
Qy 243 rLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLeuProValLysGlyAs 263  
Db 968 AGAAGAGATGAATGTATCAGTGTGTGGCTTATACATATGGGAAGCCTGTCCCTGGACA 1027  
Qy 263 pValThrLeuThrPheLeuProLeu----- 271  
Db 1028 TGTACTGTGAGCATTGCGAAGATAGTAGTACGCTTCCGACTGCCACGGTGAAGATTC 1087  
Qy 272 -----SerPheTrpGlyLy 276  
Db 1088 ACAGGCTTCTGTGAGAAATTCAGTGACAGCTAAACAGCCATGGCTGCTTCTATCAGCA 1147  
Qy 276 sLysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAs 296  
Db 1148 AGTAAATA---ACCAGGTCTTCCAGCTGAAGAGG-----AAGGA 1183  
Qy 296 pGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSe 316  
Db 1184 GTATGAATGAAA-----CITCACACTGAGGCCACAGATCCA 1219  
Qy 316 rSerProGlyProValGluIleLeuThr-----ThrValThrGluSerVa 331  
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Qy 351 eGluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrVally 371  
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Qy 371 sValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluAtrgArgAsnAsnValIle1 391  
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Qy 391 eThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnly 411  
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Qy 411 sMetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPh 428  
Db 1442 GCATGGCCTTGTACAGTCTCTATCAACACCACCAATGTTATGGGTACCTCTCTTACTGT 1501  
Qy 428 eLysIleGluPhePro-----IleLeuGluAspSe 438  
Db 1502 TAGGGTCAATTACAGGATCGTAGTCCCTGTTACGGCTACCATGGGTGTCAGAGAACA 1561  
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Qy 492 gLeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGI 510  
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Qy 510 Y-----LysGlnAsnSerThr-----MetPheSerLeuTh 520  
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Qy 580 lThrGlnProAspSerIleValGlyIleAlaValAspLysSerValAsnLeuMetAs 600  
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Qy 619 rGlyTyr-----TyrLeuGlyMe 625  
Db 2123 TGGCTTCCCTGGGCTTTGAAATGACAGGACGACGATGATCAATCAATGCTCATATGT 2182  
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Qy 660 rAlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLe 680  
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Db 2415 -----CCTCACAGGAGACCGTACGAAAGTACTTCCCTGAGACATGGATCTCGGA 2464  
Qy 697 uAspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerI1 717  
Db 2465 TTTGGTGTGTAAACTCAGCAGGTGGTGGTAGGAGTAGGAGTAAACATCCCTGACACCAT 2524  
Qy 717 eThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrTh 737  
Db 2525 CACCGAGTGAAGGACGAGGCGCTTCTGCTGTCTGGAAGATGCTGGACTTGGTATCTCTTC 2584  
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Db 2585 CACT---GCCTCTCTCCAGCCTTCCAGCCCTCTTTGTGGAGCTCACATGCTTACTC 2641

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DB	2642	TGTGATTCTGTGGAGAGCCTTTCACATCAAGGCCAGCGTCTTAACATTACCTTCCCAAATG	2701
QY	777	aThrGluValIysValIleIleGluIysSerAspLysPheAspIleuMetThrSerSe	797
DB	2702	CATCCGGGTGAGTGTGAGCTGGAGAGCCTCTCCGCCCTTCTAGCTGCCAGTGGAGAA	2761
QY	797	rGlu-----IleAsnAlaThrGlyHisGlnThrLeuLeuValProSe	812
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DB	2802	-----ACTGTGCTCTGGGAGTAAACCCCAAGTCATTAGGAATGTGAATTT	2848
QY	832	eThrValThrAlaLeuSer-----ProThrAl	841
DB	2849	CATGTTGAGCGCAGAGCAGCTAGAGTCTCAAGAGCTGTGTGGAGCTGAGTGTGCTTCAGT	2908
QY	841	a-----SerAspAlaValThrGlnMetIleLeuValIysAlaGluGlyIl	856
DB	2909	TCTTGAACCGGAAGAAACACAGATCAAGCCTCTGTGTGGTGTGAACCTGAAGAGCT	2968
QY	856	eGluIysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerTh	876
DB	2969	AGAGAAGAAACAACATTCACCTCCCTACTTTGTCCATCAGTGGTGGTCTCTCT	3023
QY	876	rLeuIysThrLeuSerPheSerPheProProAsnThrValThrClySerGluArgValGl	896
DB	3024	-----GAAGAATATCCCTGAAACTGCCACCACAAATGTGTAGAAGAAATCTCCCGAGGCTC	3079
QY	896	nIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleAr	916
DB	3080	TGTCCTCAGTTTGGAGACATATTAGGCTCTGCCATGCCAAACACACAAAATCTTCTCCA	3139
QY	916	gMetProTyrClyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLe	936
DB	3140	GATGCCCTATGGCTGTGGAGAGAAATATGTGCTCTTTGTGCTCTAACATCATGTGACT	3199
QY	936	uAspTyrLeuThrIlysIysLysGlnLeuThrAspAsnLeuIysGluIysAlaLeuSerPh	956
DB	3200	GGATTATCTAAATGAACACAGCAGCTTCCTCCAGAGATCAAGTCCAAGSCCATTTGGCTA	3259
QY	956	eMetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAl	976
DB	3260	TCTCAACACTGGTTTACCAGAGACAGTTGAAGTCAAAACACTATGATGGCTCTCTACAGCAC	3319
QY	976	aPheGly---AsnTyrAspProSer---GlySerThrTyrLeuSerAlaPheValLeuAr	994
DB	3320	CTTTGGGAGCGGATATGGCAGGACACGAGCGCAACACTGGCTCACAGCTTTGTTCTGAA	3379
QY	994	gCysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTy	1014
DB	3380	GACTTTTGGCCCAAGCTCGAGCCCTACATCTTCATCGATGAAGACACATTAACCAAGCCCT	3439
QY	1014	rThrTyrLeuIysGlyHisGlnIysSerAsnGlyGluPheTyrAspProGlyArgValIl	1034
DB	3440	CATATGGCTCTCCAGAGGCGAAGGACATGCTGTTTCAGAGGCTCTGGGTCACTGCT	3499
QY	1034	eHisSerGluLeuGlnGlyGlyAsnIysSerProValThrLeuThrAlaTyrIleValTh	1054
DB	3500	CAACAATGTCATAAAGGAGGAGGTAGAAGATGAAGTGAACCTCTCCGCCCTATATCACCAT	3559
QY	1054	rSerLeuLeuGlyTyrArgIlystYrGlnProAsnIleAspValcIlnGluSerIleHisPh	1074
DB	3560	CGACCTTCTGGAGATTCTCTCAGATCACTACCCCTGTTGTTCGGCAATGCCCTGTTTTC	3619
QY	1074	eLeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrTh	1088
DB	3620	CCTGGAGTCAAGCTGGAAGACAGACACAAGAAAGGGACATGGC---AGCATGTATATAC	3676

Qy	1088	rLeuAlaLeuIleThrTyrAla-LeuSerSerValGlySer---ProLysAlaLysGluA	1107
Db	3677	CAAAAGCACTTCCTGGCCCTATGCTTTTCCCTGGCCAGGTAACACGAGCAACAGAGAAAGG	3736
Qy	1107	laLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyMetGlnPheTrp-----	1124
Db	3737	TACTCAAGTCACATTAAATGAGRAAGCTGTGAAGAAGACAACCTCTGTCCATTGGGAGCGCC	3796
Qy	1125	--ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspI	1142
Db	3797	CTCAGAAACCAAGGACGACAGTGGGGCATTTTACGAACCCCAAGGCTCCCTCTGCTGAGG	3856
Qy	1142	leGluValAlaIaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrS	1159
Db	3857	TGGAGATGACATCTATGTGCTCTCGCT--TATCTCAGGCGCCAGCCAGCCCCAACCT	3913
Qy	1159	erGluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerL	1175
Db	3914	CGAGGACCTCGACCTCTGCACCAACCAATCGTGAAGTGGATCAGAAAGCAGCAAGATGCC	3973
Qy	1175	eugGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheA	1195
Db	3974	AGGCGGTTTCTCTCCACCCAGACACAGTGTGGCTCTCCATGCTCTGTCCCAATATG	4033
Qy	1195	laAlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerP	1215
Db	4034	GAGCAGCCACATTATACC--AGGACTGGGAAGCTGCACAGGTGACTATCCACTCTTCAG	4090
Qy	1215	roSerProLeuAlaValValGln-----	1222
Db	4091	GGACATTTCCAGCAAAATCCAGTGGACAACAACCCGCTGTACTGCAGCAGGTCT	4150
Qy	1223	-----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleC	1238
Db	4151	CATTGGCAGAGCTGCCTGGGAAATACAGCATGAAGTGCAGAGGAAGGTGTGTCTACC	4210
Qy	1238	ysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerI	1258
Db	4211	TCACAGATCTTGAATACAAATATT-----	4237
Qy	1258	leGlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysA	1275
Db	4238	TCCAGAAAGGAAGAGTTCCTCTTTGCTTTAGAGTGCAGACTCTGCCTCAAACTGTG	4297
Qy	1275	spAspLeuAsn--HisValAspLeuAsnValCysThrSerPheSerGlyProGly---	1292
Db	4298	ATGACCCCAAGCCACACCCAGCTTCCAAATCTCCCTAGTGTCTACACAGGAGGCC	4357
Qy	1293	-----ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProS	1311
Db	4358	GCTCTGCTCCACATGGCGATCGTTGATGTGAAGATGTCTCTCGCTTCATTCCTCGTGA	4417
Qy	1311	erGluAlaIleSerLeu-----SerGluThrValLysLysValGluTyrAspHisG	1328
Db	4418	AGCCAACAGTGAATAATGCTTGAAGAATCTAACCATGTGAGCCGGACAGAGTCAGCAGCA	4477
Qy	1328	lyLysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProA	1348
Db	4478	ACCATGCTTTGATTTACTTGTATGAAGTGTCAATCAGACACTGAGCTGTTCTTCACGG	4537
Qy	1348	laValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrT	1368
Db	4538	TTCTGCAAGATGCCAGATGAAGATCTGAAACACGCCATAGTGAAGTCATGATTACT	4597
Qy	1368	yrGluProArgArgGlnAlaValArgSerTyrAsnSer	1380
Db	4598	ACGAGACGATGAGTTTGCAATTTGCTGAGTACAATGCT	4635

RESULT 4  
US-09-016-434-1174  
; Sequence 1174, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:

APPLICANT: Janice Au-Young  
 APPLICANT: Jeffrey J. Selhamer  
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 NUMBER OF SEQUENCES: 1490  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/016,434  
 FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1174:

SEQUENCE CHARACTERISTICS:

LENGTH: 4079 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g177869

US-09-016-434-1174

Alignment Scores:  
 Pred. No.: 6,71e-135 Length: 4079  
 Score: 1346.50 Matches: 419  
 Percent Similarity: 46.66% Conservative: 238  
 Best Local Similarity: 29.76% Mismatches: 488  
 Query Match: 18.32% Indels: 263  
 DB: 4 Gaps: 54

US-10-020-095-4 (1-1428) x US-09-016-434-1174 (1-4079)

QY 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31  
 Db 86 CTCTTGCTGCTCCCTGCCACAGACGGCTCAGTCTCTGGAACCCAGGATATATGTTCTG 145  
 QY 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51  
 Db 146 GTCCCTCCCTGCTCCACACT---GAGACACTGAGAGGGCTGTCTCTCTGAGCTAC 202  
 QY 52 CysProSerGlnValThrValValAlaGluLeuLysThrAlaSerAsnLeuThrVal 71  
 Db 203 CTGAATCAGACAGTGTAGTGTCTCTGAGTCTCTGAGTCTCTGAGGGAACAGGACCTC 262  
 QY 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89  
 Db 263 TTCCTGACCTGGAGGGGAGATGAGTACTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 310  
 QY 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleYrGluLeuArgVal 106  
 Db 311 -----CTGTGCCAAAGTCTTCATCCATGAGGAGGATATGTTCTCTCACTGTCCTCAAGTG 364

QY 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126  
 Db 365 AAAGGACCAACCCCAAGAA-----TTTAAGAAGCGGACACAGTGTGGTTAAGAAC 415  
 QY 127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146  
 Db 416 GAGGACAGTCTGGTCTTTTCCAGACACAAATCATCATCAACACGAGGCGACAGTG 475  
 QY 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166  
 Db 476 AAATTCGTGTGTCTCCATGGATGAAACTTTCCACCCCTGAATGAGTTGATTCACATA 535  
 QY 167 Leu---IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnSerAsp 185  
 Db 536 GTATACATTCAAGATCCCAAGAAATCGCATGCACAATGGCAGAGTTTCCAGTTAGAG 595  
 QY 186 LeuGlyValIleSerLysThrPheGlnSerHisProIleLeuGlyAspTrpSer 205  
 Db 596 GGTGGCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTCCAGGGCTCCTACAAG 655  
 QY 206 IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu 223  
 Db 656 GTGGTGTACAGAAAGAAATCAGGTGGAAGGACAGACAC---CCTTTACCCGTGGAGAA 712  
 QY 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243  
 Db 713 TTTGTTCTTCCCAAGTTTGAAGTACAGTACAGTGCCTCAAGATAATCACCATCTTGAA 772  
 QY 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263  
 Db 773 GAAGAGATGAATGATCAGTGTGTGGCTATACACATATGGAAGCTGTCTCCCTGGACAT 832  
 QY 264 ValThrLeuThrPheLeuProLeu-----271  
 Db 833 GTGACTGTGAGCATTTGCAGAAAGTATAGTACGCTCCGACTGCCACGCGTGAAGATCA 892  
 QY 272 -----SerPheTrpGlyLys 276  
 Db 893 CAGGCTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTCTCTATCAGCAA 952  
 QY 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296  
 Db 953 GTAAAA-----ACCAAGGTCTTCCAGCTGAAGAGG-----AAGGAG 988  
 QY 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316  
 Db 989 TATGAATGAAA-----CTTCACACTGAGGCGCCAGATCCAA 1024  
 QY 317 SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal 331  
 Db 1025 GAAGAAGGAACAGTGTGGAATTCAGTGGAGGCGAGTCCAGTGAATCAACAGAACCAT 1084  
 QY 332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351  
 Db 1085 ACCAACTCTCA---TTTGGAAGTGTGACTCACACTTTGACAGGGA-----ATT 1132  
 QY 352 GluPhePheAspTyrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371  
 Db 1133 CCTTCTTTGGG-----CAG 1147  
 QY 372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsnValIle 391  
 Db 1148 GTGGCCCTAGTAGTGAAGAGGCGTCCCTATACCA-----ATAAAGTCATA 1195  
 QY 392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411  
 Db 1196 TTCATC---AGAGAAATGAAGCAAACTATTAC-----TCCAATGTCTACCCAGGATG 1246  
 QY 412 MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe 428  
 Db 1247 CATGGCTTGTACAGTCTCTTATCAACACCACCAACGTTATGGTACTCTCTTACTGTT 1306  
 QY 429 LysIleGluPhePro-----IleLeuGluAspSer 438

1307 AGGTCATTAACAGGATCGTAGTCCCTGTATCGCTACAGTGGGTGTCAGAAGAACAC 1366  
 439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSer 458  
 1367 GAAGAGGCACATCACATGCTTAT----- 1390  
 459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478  
 1391 CTGTGTCTCCCAAGACAGAGCTTTGTCCACCTTGAGCCCATGTCTCATGAACATACC 1450  
 479 ValGlySer-----ProPheGluLeuValValSerGlyAsnLys-----Arg 492  
 1451 TGTGGCCATCTACAGACAGTCCAGGCACATATATCTGAATGAGGCACCCCTGCTGGG 1510  
 493 LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly 510  
 1511 CTGAAGAAGCTCTCTTTTATCTGATATGTAATGCAAGAGGCGCATTTGCCAACTGGG 1570  
 511 -----LysGlnAsnSerThr-----MetPheSerLeuThr 520  
 1571 ACTCATGGACTGTTGTAAGCAGGAGACATGATGAAGGGCCATTTTCCATCTCAATCCCT 1630  
 521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540  
 1631 GTGAAGTCACACATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1690  
 541 GluIleSerValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560  
 1691 GAGCTGATGGGATTCGCAAAATATGATGTTGAAATTTGTCGCCAACAGGTGGAT 1750  
 561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580  
 1751 TTGAGCTTCAGCCCATCACAAAGTCTCCAGCTCCACGCCCTCACAGCCCATCTGGAGTCA 1810  
 581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600  
 1811 GCT---CCTCAGTCCGTCTGCGCCCTCGGTGCTGTGACCAAGCTGTGCTCATGAAG 1867  
 601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeu---GluLeuTyrAsnThr 619  
 1868 CTGTGCTGAGTCTGCGCGTCTCGGTTCACACCTGCTACCAAGAGGACCTCACT 1927  
 620 GlyTyr-----TyrLeuGlyMet 625  
 1928 GGCTTCCTCGGCTTTGATGACAGGAGGATGAGATGTCATCATCTCATATGTC 1987  
 626 PheMetAsnSer-----PheAla 631  
 1988 TATATTAATGGAATCATATATCTCCAGTATCAAGTACAAATGAAAGGATATGATACAGC 2047  
 632 ValPheGlnCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651  
 2048 TTCCTAGAGACATGGGCTTAAGGCATTCACCACTCAAGATTCGTAAACCCCAAAATG 2107  
 652 AspGlyValTyrAspAsnAlaGlu-----Tyr 660  
 2108 TGTCACAGCTTCAACAGTATGAATGATGACCTGAGGCTACGCTAGTGTATTTAT 2167  
 661 AlaGluArgPheMetGluGlnGlnGlyHisIleValAspIleHisAspPheSerLeu 680  
 2168 GAGTCAGATGTAATGGGAAGAGGCCATGACGCCCTGGTGCATGTTCAAGAG----- 2218  
 681 GlySerSerProHis-----ValArgLysHisPheProGluThrTrpIleTrpLeu 697  
 2219 -----CCTACAGGAGCCGTACGAAGTACTTCCCTGACACATGATCTGGGAT 2269  
 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717  
 2270 TTGGTGGTGAATCAACTCAGCAGGGGTGGCTGAGGTAGGATTAACAGTCCCTGACACCATC 2329  
 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuThrThr 737

2330 ACCGAGTGAAGCGGAGGCGCTTCTGCTGCTGAAGATGCTGAGCTTGGTATCTCTTCC 2389  
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 758 ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777  
 2447 GTGATTCGTGGAGAGGCTTTCACATCAAGGCCAGGTCCTAAACTACTCTTCCCAATGC 2506  
 778 ThrGluValLysValIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797  
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 2606 -----ACTGTCTCTGGCAGTAAACCCCAAGTCATTAGGAATGTGAATTC 2653  
 833 ThrValThrAlaLeuSer-----ProThrAla 841  
 2654 ACTGTGAGCGCAGAGGCGCATAGTCTCAAGAGTGTCTGGAGCTGAGGTGCTTCACTT 2713  
 842 -----SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856  
 2714 CCTGAACACGGAAGAAAGACACAGTCATCAAGCTCTGTTGTTGAACCTGAGGACTA 2773  
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 2774 GAGAGGAACAACAACACTCACTCTTGTCTCATCAGCTGTGTGAGTTCT----- 2827  
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 2828 ---GAAGAAATTCCTGAAACTGCCCAAAATGTGTAGGAATCTGCCCGAGCTTCT 2884  
 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916  
 2885 GTCTCAGTTTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCAG 2944  
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 957 MetArgGlnGlyTyrGlnArgGluLeuTyrGlnArgGluAspGlySerPheSerAla 976  
 3065 CTCACACTGCTTACCGAGACAGTGAACACTACAACTATGATGCTCTCTACAGCACC 3124  
 977 PheGly---AsnTyrAspProSer---GlySerThrTrpLeuSerAlaPheValLeuArg 994  
 3125 TTTGGGAGCGATATGCGAGAACACAGGCAACACTGGCTTCAGAGCTTTGTTCTGAAG 3184  
 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014  
 3185 ACTTTGCCCAAGCTCAGGCTACATCTTCATCGATGAAGCACACATACCCAGCCCTC 3244  
 1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034  
 3245 ATATGGCTCTCCAGAGCGCAGGACATGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3304  
 1035 HisSerGluLeuGlnGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054  
 3305 AACAAATGCCATAAAGGAGGAGTAGAAGTAGAAGTGAAGTCCCTCTCCGCTATATCACCATC 3364  
 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074  
 3365 GCCCTTCTGGAGATTCTCTCACAGTCACTCACCCTGTTGTCCGAATGCCCTGTTTTC 3424

1075	LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr	1088
3425	CTGAGTCAACCTGGAGACAGACACAAAGAGGGGACCATTGSC--AGCCATGTATATATACC	3481
1089	LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProIysAlaIysGluAla	1107
3482	AAAGCACTGCTGCCTATGTCTTTTGGCTGGCAGGTAAACACGACAGAGGAAGGAAGTA	3541
1108	LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyMetGlnPheTrp-----	1124
3542	CTCAAGTCATTTAATGAGGAAGCTGTCAAGAAAGACAACCTCTCTCCATTGGGAGGCCCT	3601
1125	ValSerSerGluSerIysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle	1142
3602	CAGAAACCCAGGACACAGTGGGGCATTTTACGAACCCAGGCTCCCTCTGCTGAGGTG	3661
1143	GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer	1159
3662	GAGATGACATCCATGTGCTCTCTCGCT--TATCTCAGCGCCAGCGCCCAACCTCG	3718
1160	GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerLeu	1175
3719	GAGACCTGACCTCTGCAACCAACATCGTGAAGTGGATACGAAGACGACGAATGCCAG	3778
1176	GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuIysAlaLeuSerGluPheAla	1195
3779	GGCGTTTCTCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGA	3838
1196	AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro	1215
3839	GCGCCACATTTACC--AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG	3895
1216	SerProLeuAlaValValGln-----	1222
3896	ACATTTCCAGCAAATTTCCAAGTGGCAACAACAATCGCTGTGTACTGCACGAGGTCTCA	3955
1223	-----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys	1238
3956	TTGCCAGAGTGCCTGGGGAAATACAGCATGAAGTGCACAGAGAGGATGTGTCTACCTC	4015
1239	GlnLeuAsnValValTyrAsnVal	1246
4016	CAGACCTCTTGAATATCAATATT	4039

## RESULT 5

US-08-447-411-1  
; Sequence 1, Application US/08447411  
; Patent No. 5773243  
; GENERAL INFORMATION:  
; APPLICANT: FRITZINGER, DAVID C.  
; APPLICANT: BREDEHORST, REINHARD  
; APPLICANT: VOGEL, CARL-WILHELM  
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,411  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

Db 528 AGTTCTAAACAGCTCAATCCATCAGCTCGATCCGGCCCTTACAATTTACCAGAGCTTGTC 587  
QY 201 ---LeuGlyAspTrpSerIleGlnValGlnValAsn-----AspGlnThrTyrTyr 216  
Db 588 AGTTTGGGACATGGAAGCTGGGCCAAATATGAACATTCACCAGAGAGCTACACT 647  
QY 217 GlnSerPheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrPro 236  
Db 648 GCATATTTTGTATCAGAGAAATATGTTTACCAAGCTTTGAAGTCGCTGCAACCATCA 707  
QY 237 -----LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLys 253  
Db 708 GATAAGTTCTTTACATTGATGGGAAT---AAAATTTCCAGTGTCTATCATCTGCAGG 764  
QY 254 TyrThrTyrGlyLysProValLysGlyAspValThrLeuThrPheLeuProLeuSerPhe 273  
Db 765 TACTTATATGGAAGAAAGTGAAGCT---GTGGCCCTTTGTCTCTTTGGAGTCAAAATA 821  
QY 274 TrpGlyLysLysAsnIle-----ThrLysThrPheLysIleAsnGlySer 289  
Db 822 GATGATGCTAAAGAGATATTCAGACTCACTCAGAGAAATCCGATTAATTGATGGAGAT 881  
QY 290 AlaAsnPheSerPheAsnAspGluMetLysAsnValMetAspSerSerAsnGlyLeu 309  
Db 882 GGGGAAGCAACACTAAAGAGATACACTACGTTCCCGATTTCAAGATCTCAATCAGCTT 941  
QY 310 SerGluTyrLeuAspLeuSerSerProGlyProValGluIleLeuThrValThrGlu 329  
Db 942 GTTGGTCATCTCTGTATGTATCT-----GTAACAGTGAACAGAA 983  
QY 330 SerValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyr 349  
Db 984 TCAGGAGTGAATGTAGTACTGAGCAAGCGGCATTTCATATTGTGACATCTCCCTAT 1043  
QY 350 IleIleGluPhePheAspTyrThrThrValLeuLysProSerLysAsnPheThrAlaThr 369  
Db 1044 CAGATCTACTTCCAAAAACCCCAAAATATTTCAGCCAGGAATGCCATGAATCGACG 1103  
QY 370 ValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgAsnVal 389  
Db 1104 GTGTATGTACCAACCTGATGCTCACCAGCTGCC-----CAT 1142  
QY 390 ValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsn 409  
Db 1143 GTCCAGTGTATCAGAGGCCATTTCATCTTGAG-----GGAACC 1181  
QY 410 GlnLysMetGluAlaValGlnLysIleAsnTyrThrValPro-----GlnSerGly 426  
Db 1182 ACTTTGAGTATGGGACTGCTAAGCTCATCTGAAACACCACTGAACATTCANAAGC--- 1238  
QY 427 ThrPheLysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyr 446  
Db 1239 -----CTACCGATCACTGTAGNACTAACCATGGAGACCTCCAGAGAA 1283  
QY 447 PheLeuGlySerLysSerMetAlaValHisSerLeuPheLysSerProSerLysThr 466  
Db 1284 CGCCAGGCAATAAAGTCCATGACAGCCACAGCCCTACCAACCCAGGCGGTCTGAAAC 1343  
QY 467 TyrIleGlnLeuLysThrArgAspGluAsnIleLysValGlySer-----ProPheGlu 484  
Db 1344 TATCTTTATGATGCCATTACATCTACAGAGATTAAAGCCCGGAGATTAATCTGTCAAT 1403  
QY 485 LeuValValSerGlyAsn-----LysArgLeuLysGluLeuSerTyrMetVal 500  
Db 1404 TTCAATGTGAGGGCAATGCAAAATTCATCAACCATCAATATTTACATACCTCAT 1463  
QY 501 ValSerArgGlyGlnLeuValAlaValGlyLys-----GlnAsnSer 514  
Db 1464 TTGAATAAAGGGAAGATTTCAGGTTGGCAGCAACCCAGGAGAGATCGGCAGATCTG 1523  
QY 515 ThrMetPheSerLeuThrProGluAsnSerThrProLysAlaCysValIleValTyr 534

Db 1524 GTGACCATGAATCTGCATATCACTCCAGATCTCATCCCTTCCGTTTGTGGCTTAC 1583  
QY 535 TyrIleGluAspAspGlyGluIleSerAspValLeuLysIleProValGln----- 552  
Db 1584 TACCAAGTGGGAATAAAGAAATGTGGCTGATTCTGTCTGGGTGGATGTGAAGATACC 1643  
QY 553 -----LeuValPheLys-----AsnLysIleLysLeuTyr 562  
Db 1644 TGCATGGGAAGCTTGGTTGTGAAGAGGAGCGCTTCCAGACAGCATCAATACAA- 1697  
QY 563 TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582  
Db 1698 -----AAGCCAGAGCTGCATGAATCAAAATTGGA----GGGGAT 1736  
QY 583 ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer 602  
Db 1737 CCAGTGTCTCGGGTGTGTTGTGGCTGTGGACAAGCAGTATATGTCTCAATGATAAA 1796  
QY 603 AsnAspIleThrMetGluAsnValHisGluLeuGluLeuTyrAsnThrGlyTyrTyr 622  
Db 1797 TATAAGATTAGCAAGCTAGATATGGGACACATAGAAAAGATGACTTTGGCTGTACA 1856  
QY 623 LeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTyrValLeuThr 642  
Db 1857 GCTGCGAGTGGCCAGAAATAATCTGGGTGTGTTTGAAGATGCTGAGCTGGCTCTGACAACC 1916  
QY 643 AspAlaAsnLeuThr----- 647  
Db 1917 AGCACTAATCTCAACACCAACAGAGATCAGCTCAAGTGTCTCAGCTGCCAATCGG 1976  
QY 647 ----- 647  
Db 1977 AGCGTGCAGCTTCTGTTTCTGCTTTCAGACAAAGCAAGCAAGCGGCACAGTTTCAG 2036  
QY 648 -----LysAspTyrIleAspGlyValTyrAspAsn----- 657  
Db 2037 GATCAAGCCCTCGCTAAATGCTGTGAAGATGGCATGTCATGAGAACCCTCATGGGTACT 2096  
QY 658 AlaGluTyrAlaGluArgPheMetGluGluAsnGluGly----- 670  
Db 2097 TGTGNAAGCGTGCAAAATATACATCCAGGAGGAGATGCTTGTAAAGCTGCCTTCCTTCAA 2156  
QY 671 -----HisIleVal----- 673  
Db 2157 TGTGTCTACTACATCAAAAGGATCCGAGATGAAACCAACCGGAGAGCGAGTCTTCTTG 2216  
QY 674 -----AspIleHisAspPheSerLeuGlySerProHisVal---ArgLysHis 689  
Db 2217 GCAGAAGTGAATTTTGAAGATGAATCTTTGGAGATGACACATCTCCAGTCTGAT 2276  
QY 690 PheProGluThrTrpIleTrpLeu-----AspThrAsnMetGly 702  
Db 2277 TTTCCGAGAGCTTGGTTGTGGCTAACAGAGGAATTGACCGGGAGCCTAACAAATCAAGG 2336  
QY 703 TyrArgIleTyrGlnGluPheGluValThrValPro-----AspSerIleThr 718  
Db 2337 ATTTCA-----AGCAAGACAGTACCTTTTATCTGAGGGATTCATCACA 2381  
QY 719 SerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 738  
Db 2382 ACCTGG-----GAGTGTGCTGGGCTTTTCCACCACC 2417  
QY 739 -----ProValGluLeuGlnAlaPheGlnProPhePheIlePhe 751  
Db 2418 AAAGGATCTGTGTGGCTGAACCTGTATGAATAACAGTCATGAAGAGCTTCTTCATTGAT 2477  
QY 752 LeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePhe 771  
Db 2478 CTTTGACTGCCATATTAGTAGTGAAGATGAGCAGGTGGAGATTCGAGCTATTCTGTAC 2537  
QY 772 AsnTyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAsp 791  
Db 2538 AACTACGCTGACGAGGATATTTATGTGCGAGTGAACCTGATATACACCCAGCCTTC--- 2594

QY	792	IleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValPro	811
Db	2595	-----TGCAGTGGCTTCCACAGAGGACAAAGATACCAGACGAGTTC	2645
QY	812	SerGluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly	829
Db	2646	GCCTGTCCTCCAGACGACATACCATTGTGATAGTCCATTAGACGAAGATTGCATGAT	2705
QY	830	IleProIleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIle	849
Db	2706	GTTGAGGTTATACCAAGTGTCCGGGAGAGTTGGCATCAGATGGTGTGAGGAAGAACTG	2765
QY	850	LeuValIysalaGluGlyIleGluIysSerTyrSerGlnSerIleLeuLeuAspLeuThr	869
Db	2766	AAAGTTGTACCTGAAGGGGACGGAAATAATTGTGACTATATTATGAACATGGACCCCAAGT	2825
QY	870	AspAsnArgLeuGlnSerThr-----LeuLysThrLeuSerPheSerPheProAsn	887
Db	2826	GTAAGAAGGAGTGGTGGAAACCCAGGAACTAACGGTCATACCCCAATAAATAGATGACAAG	2885
QY	888	ThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAsp	903
Db	2886	GTCCCTCATACAGAAGTTGACACGAGATTCTGTTCTAGTGACCCCTGGGCTCAGATT	2945
QY	904	LeuGlyProSerIleAsnGly-----LeuAlaSerLeuIleArgMetProTyrGlyCys	921
Db	2946	ATTGAAACCTCAATTGATGGAAGTAAACTCAATCATCTCATTATTACTCTCTGGCTGT	3005
QY	922	GlyGluGlnAsnMetIleAsnPheAlaProAsnIle-----TyrIleLeuAspTyr	938
Db	3006	GGGAGACAAATATGATACCATGCTCCATCGGTATGCCACCTACTACTTTGGACGCA	3065
QY	939	LeuThrLysLysLysGlnLeuThrAspAsnLeuLysLysAlaLeuSerPheMetArg	958
Db	3066	ACAGGCGAGTGGGAGAACTCTGGTGGATCGCAGGAGTGAAGCTATCAACAGATCATG	3125
QY	959	GlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGly	978
Db	3126	ACTGGTTATCCCGACAGATGGTGTACAGAAAGACAGATCATTTCCATGCGAGATTACA	3185
QY	979	AsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGlu	998
Db	3186	AAC-----CGTGCATCTAGTCTTGGCTAACAGCATATGTGGTGAAGTCTTAGCCATG	3239
QY	999	AlaAspProTyrIle---AspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu	1017
Db	3240	GCATTCCAACATGTTAAAGACATTAGCCATGAATATTATTGTGGAGGTGTGAATGGCTC	3299
QY	1018	--LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSer	1036
Db	3300	ATTCTGAACAGGCAACACCAGATGGAGTGTTCAAGAAAAATGCCCTGTGATCCATGGA	3359
QY	1037	GluLeuGlnGlyGlyAsnLysSer-----ProValThrLeuThrAlaTyrIleVal	1053
Db	3360	GAATGCTGGGAGGAACATAAGGTGTGTAACCAAGACGATCTTTAAACAGCATTCATTGTG	3419
QY	1054	ThrSerLeuLeuGlyTyrArg-----LysTyrGlnProAsnIle-----Asp	1067
Db	3420	ACTGCAATTATGGAATCCAGATCAGTCTGCAAGAACAAATCATATTCTAGACAGCAGC	3479
QY	1068	ValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyr	1087
Db	3480	ATCAATAAGGCCACAGATTATTTACTCAAAAGATATGAGAAA---CTGCAAGAGCCCTTAC	3536
QY	1088	ThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla	1107
Db	3537	ACTACAGCCCTCACGCCATGTGTTGGCT-----GCTGACAGCCGA	3578
QY	1108	LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheThrValSerSer	1127
Db	3579	CTCAATCATGACAGGGTACTCATGGCAGCATCAACAGGAGGAATCGTTGG-----	3629

Qy	1128	GluserylserLeuserAspSerTrpGlnProArgSerLeuAspIleGluValAlaIleTyr	1144
Db	3630	-----GAGAAATAATATGCTCGCAGCCATAATAATTAAGGCACTTCCTCAT	3674
Qy	1148	AlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrp	1167
Db	3675	GCCTTGTGGCCCTGCGAAAAATTCAGAAATTTGCTGAGGTGGTCTGTAGTCAGATGG	3734
Qy	1168	LeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAla	1187
Db	3735	CTGATAGATCAGAAAAATATTATGGGGGAACATATGGCAAAACCCCAAGCAACAGTATGGTG	3794
Qy	1188	LeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArg--ThrAsnIleGln	1206
Db	3795	TTTCAAGCTCTTGCTGNAATATGAGATTCAGATGCCTTACCCATCAGGACTTAAATTTAGAT	3854
Qy	1207	ValThrValThrGlyProSerSerProSerPro-----LeuAla	1219
Db	3855	ATTTCTTAACTGGCAGAACAGAGAGTACCTCGAAAGGTACAGCAATTAAATGATGAAAT	3914
Qy	1220	ValValGlnProMetAlaVal-----AsnIleSerAlaAsn	1231
Db	3915	GCTGTCCAGGCCCGACAGTAGAGACCAAACTCAACGAAGACTTCATGTGTGTCAGCATCA	3974
Qy	1232	GlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySer	1251
Db	3975	GGTGATGGAAAGCAACAATAGCCATTTTGACGGTCTATAATGCACAATTG-----	4025
Qy	1252	SerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaVal---	1270
Db	4026	---AGGAGAGATCCAAATGTTTCCACAAA-----TTCCATCTTGATGTTCTGTGTAA	4076
Qy	1271	-----LysGluAsnLysAspAspLeuAsnHisValAspLeuAsnVal	1284
Db	4077	AACGTCCGAATTGAACTTTAAACAGGCAAGGGAGGCAAGCGACCCCTCAGGTTTAAATC	4136
Qy	1285	CysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeu	1304
Db	4137	TGCACTAGGTATCTGGGAGAGTTGATCTTCAATGACAATAATTGATATTTCTATGCTG	4196
Qy	1305	SerGlyPheMetValProSerGluAlaIle-----SerLeuSerGluThr	1319
Db	4197	ACTGGTTTTTTCCTGATGCTGAAGACCTTAAAGGCTTCTAACGGATGGAGCATAC	4256
Qy	1320	ValLysLysValGluTyrAspHis-----GlyLysLeuAsnLeuTyrLeu	1334
Db	4257	ATCTCCAGTTTGAAATTCACAATAATATGGCTCAGAAAGGAACCTGTGTCACTTACTTA	4316
Qy	1335	AspSerValAsnGluThrGln---PheCysValAsnIleProAlaValArgAsnPheLys	1353
Db	4317	GACAAGTCTCCCACTCTGAAGATGAATCCCTGCATTTTAAGATTCAACAGCAATTTGAA	4376
Qy	1354	ValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGln	1373
Db	4377	GTTGGCTTCATTCAGCCAGGATCAGTCAAGGTGTACAGCTACTACAATCTAGATGAACAA	4436
Qy	1374	AlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspVal	1393
Db	4437	TGTACCAAGTTCTACCATCCAGATAAAGAAACAGGTCTTCTCAATAGATATGTCATGGT	4496
Qy	1394	GlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHisHis-----	1409
Db	4497	AACATTGGCGATGTCAGAGAAGAACTGTGTTCTTCTCAACCAGCAGAAAAAAGATTGAT	4556
Qy	1410	-----SerSerValIlePheIlePheCysPheLys	1419
Db	4557	CTTCAATTACGAANTCAAAAGCCTCGCGCAAAATGTGGATTGTCTCAAAACCAAG	4616
Qy	1420	LeuLeu-----TyrPheMetGluLeu	1426
Db	4617	CTGCTTCGAATAGAAAGAAAGATGTAAATGATATCTATTTTCATGATGTT	4667





Db	2375	GAGACTTGAAAGAGCCACCGAAATAATCTTACGAAGCTC-----	2419
Qy	707	GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal	726
Db	2420	-----ATGAATATATTTTGAAAGACTCCATCACCACGTGGGAGATTCTGGCTGTGAGC	2473
Qy	727	IleSerGluAspLeuGlyLeuThrThrProValGlnLeuGlnAlaPheGln	746
Db	2474	ATGTCGCAAGAAAGGGATC---TGTGTGGCAGACCCCTTCGAGTGCACAGTAATGCAG	2530
Qy	747	ProPhePheIlePheLeuAsnLeuProTyTrSerValIleArgGlyGluGluPheAlaLeu	766
Db	2531	GACTTCTTCATGACCTGGCGCTACCTACTCTGTTGTCGAAACGAGCAGGTGGAATC	2590
Qy	767	GluIleThrIlePheAsnTyLeuLysAspAlaThrGluValLysValIleIleGlu---	785
Db	2591	CGAGCCGTTCTCTACAATAC--CGCGAACAACAAGAGCTCAAGGTGAGGTGGAACTA	2647
Qy	786	--LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis	804
Db	2648	CTCCACATCCAGCTTCTGCACCTTGGCACCAACCAAGAG-----CGTCAC	2695
Qy	805	GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProfileArgPro	824
Db	2696	CAGCAGACCATAACCATCCCCCAAGTCCTGTTGTCCTCATATGTCATCGTGGCG	2755
Qy	825	-----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer	842
Db	2756	CTAAGACCGCGCTCGAGGAAGTGAAGTCAAGCTGCTGTCTTACCATCATTTTCATCAGT	2815
Qy	843	AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyTrSerGln	862
Db	2816	GACGGTGCAGGAAGTCCCTGAAGTCTGTCGCGAAGGAATCAGAATGAACAAACTGTG	2875
Qy	863	SerIleLeuLeuAspIleThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu	880
Db	2876	GCTGTT---GCGACCTGGATCCAGAACGCTGGCGCGTGAAGGAGTGCAGAAAGAG---	2929
Qy	881	SerPheSerPheProAsnThrVal-----ThrGlySerGluArg	894
Db	2930	-----GACATCCACTGCAGACCTCAGTGACCAAGTCCCGGACACCGAGCTGAGACC	2983
Qy	895	-----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly---	910
Db	2984	AGAATTCTCTGCAAGGACCCCAAGTGGCCCATGACAGAGGATCCGCTCGACGCGGAA	3043
Qy	911	--LeuAlaSerLeuIleArgMetProTyTrGlyCysGlyGluGlnAsnMetIleAsnPhe	929
Db	3044	CGGCTGAAGCACCTCATTTGACCCCTCTGGGCTGCGGGAACAGAAATGATCGGCATG	3103
Qy	930	AlaProAsnIleTyTrIleLeuAspTyTrLeuThrLysLysGlnLeuThrAspAsnLeu	949
Db	3104	ACGCCACGCTCATCGTGTGCATTACTTGATGATAAACGAGCAGTGGGAGAAAGTTCGGC	3163
Qy	950	LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyTrGlnArgGluLeuLeu	966
Db	3164	CTAGAGAACGGCAGGGGGCTTTGGAGCTCATCAAGAGGGGTACACCAGACGCTGGCC	3223
Qy	967	TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyTrAspProSerGlySerThr	986
Db	3224	TTCAGACAACCCAGCTCTGCCTTTGCGGCTTCGTGAAACGGGCACCC-----AGCACC	3277
Qy	987	TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyTrIleAspIleAsp	1006
Db	3278	TGGCTGACCGCCTACGTGGTCAAGGCTTCTCTCTGCTGTCTCAACCTCATCCCATCGAC	3337
Qy	1007	GlnAsnValLeuHisArgThrTyTrThrTpLeu---LysGlyHisGlnLysSerAsnGly	1025
Db	3338	TCCCAAGTCTCTGCGGGCTGTTAATGGCTGATCTCTGAGAGACGAGAACCGGACGG	3397
Qy	1026	GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGly-----	1041

3398 GTCTCCAGAGGATCGCCCGGTATACACCAAGAAATGATTGGTGATTCGGAACAC 3457  
1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061  
3458 AACGAGAAGACATGCGCCCTCAGCGCTTGTTCATCTCGTG----- 3502  
1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073  
3503 ---CAGGAGCTAAAGATATTTGCGAGGAGCAGGTCAACAGCGCTGCCAGGAGCATCACT 3559  
1074 -----PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089  
3560 AAAGCAGGAGACTTCTTGAAGCAACTAC--ATGAACCTACAGAGATCTTACATGTG 3616  
1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109  
3617 GCATTCGTGCTATGCTCTGCGCCAGATGGCAGGCTGAAGGGGCTCTTCTTAACAA 3676  
1110 MetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSer 1129  
3677 TTTCTGACC-----ACAGCC 3691  
1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAla 1146  
3692 AAAGATAAGAACCGCTGGGAGGACCTGTGTAGCAGCTCTACAACTGTGAGGCCACATCC 3751  
1147 TyrAlaLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165  
3752 TATGCGCTCTTGACC---CTATGCGAGCTAAAGACTTTGACTTTGTGCTCCCGTCGTG 3808  
1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185  
3809 CGTTGCTCAATGAACAGAGATACTACGGTGGTGGTATGGCTCTACCCAGGCCACCTTC 3868  
1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204  
3869 ATGGTGTTCAGACCTTGGCTCAATACCAAAAGAGCGCCCTGACCACCAAGCACTGAAC 3928  
1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218  
3929 CTTGATGTGTCCTTCAACTGCGCCAGCG--CAGCTCAAGATCACCCACCGTATCCACTG 3987  
1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229  
3988 GGAATCTGCCAGCTCTCGATCAGAGACCAAGAAATGAGGGTTTCACAGTCAC 4047  
1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysLase 1249  
4048 AGCTGAAGAAAGGCAAGGCCACCTTGTGGTGGTGACAATGTACCATGTCTAAGGCCAA 4107  
1249 rGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAl 1269  
4108 AGATCAACTCACTGTATAA-----TTGCACTCAAGTCTAC 4146  
1269 aVal-----LysGluAsnLysAspLeuAsnHisValAspLe 1282  
4147 CATAAAACCAGCACCGGAAACAGAAAGAGCGCTCAGGATGCCAAGACACTATGATCT 4206  
1282 uAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAs 1302  
4207 TGAGATCTTGACAGGTACCGGGAGACACGAGTGCCTATGCTATATTTGGACATATC 4266  
1302 nLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317  
4267 CATGATGACTGGCTTTGCTCCAGACAGATGACCTGAAGCAGCTGGCCAATGGTTTGA 4326  
1317 rGluThrValLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332  
4327 CAGATACATCTCAAGTATGAGTGGACAAAGCCTTCTCCGATAGAAACACCTCATCAT 4386  
1332 uTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValArgAs 1351  
4387 CTACCTGGACAAGGCTCACACCTCTGAGGATGACTGTCTAGCTTTTCAAGTTCCACCAATA 4446

QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371  
Db 4447 CTTTAATGTAGAGCTTATCCAGCTGGAGCAGTCAAGTCTTACCGCTATTACAACTGGA 4506  
QY 1371 gArgGlnAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388  
Db 4507 GGAAAGCTGTACCGGTTCTACCATCCGGAAGAGGATGGAAGCTGAACAAG----- 4561  
QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401  
Db 4562 -CTCTGCCGTGAT---GAACGTGCGCGTGTGCTGAGGAG 4597

## RESULT 7

US-09-132-271-2  
; Sequence 2, Application US/09132271  
; Patent No. 6221657  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Richard Alexander  
; TITLE OF INVENTION: FARRIES, CHARLES TIMOTHY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: United States of America  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/132,271  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US/08/793,126  
; APPLICATION NUMBER: US/08/793,126  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Hollie L.  
; REGISTRATION NUMBER: 31,321  
; REFERENCE/DOCKET NUMBER: 102286.377  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-6000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5056 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-132-271-2

Alignment Scores:  
Pred. No.: 1,2e-89 Length: 5056  
Score: 931.00 Matches: 381  
Percent Similarity: 40.88% Conservative: 287  
Best Local Similarity: 23.32% Mismatches: 609  
Query Match: 12.67% Indels: 358  
DB: 3 Gaps: 63

US-10-020-095-4 (1-1428) x US-09-132-271-2 (1-5056)

QY 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22  
Db 65 GGTCCAGCCCTGCTG-----CTCTGTACTACCCACCTCCCTGCTGCTG 112  
QY 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleIleArg----- 37

[illegible]

360 LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn--- 378  
Db TTAACACCAAGATGCCCTTTGACCTCATGGTGTCTGTGACGAACCTGATGCTCTCCA 1139  
Qy -----GlnLeuThrLeuGluGluArgAsnAsnValValIleThrValThrGlnArg 396  
Db GCCTACCGATCCCGTGGCAGTCCAGGGCGAGCACATGTGCAGTCTCTAACCCAGGGA 1258  
Qy AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln 416  
Db GATGGCGTGCCAACTCAGCATCAACACACACCCAGCCAGCAAG----- 1303  
Qy LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu 436  
Db -----CCCTTGAGCATCACGGTGCACGAAGAAGCAGGAGGCTCTCG 1345  
Qy AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaVal 456  
Db GAGCGAGAGCAG-----GCTACGAGGACCATGCAGGCTCTG 1381  
Qy HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr----- 472  
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Qy -----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn 490  
Db CTCAGACCCGGGAGACCTCAACGTCAACTTCTCTCTCGAATGAGCCGCGCCACGAG 1501  
Qy LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510  
Db GCCAAGATCGCTACTACACTACTCATGATCAAGACAGGGCAGCGTGTGAAGCGGGA 1561  
Qy Lys-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSer 524  
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Qy TrpThrProLysAlaCysValIleValTyrTyr-----IleGluAspAspGly 540  
Db TTCTCCCTTCCTCCGCTGGTGGCGTACTACACGCTGATCGGTCCAGCGGCCAGAG 1681  
Qy GluIleLeuSerAspValLeuLysIleProValGln-----LeuVal 554  
Db GAGTGTGGTCCGACCTCGTGTGGTGGACGTCAGGACTCCGTGCGTGGCTCGTGGTG 1741  
Qy PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu----- 569  
Db GTAAAAGCGGC-----CAGTCAGAAGACCCGCGAGCCTGTA 1777  
Qy ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle 589  
Db CCTGGGCGCAGATGACCTGAAGATAGAGGGTGACACCGGGCCCGGGTGGTA----CTG 1834  
Qy ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn 609  
Db GTGGCGTGACAAAGCGGTGTCGTGCTGATTAACAAGAACAACTGACCGCAGAGATAAG 1894  
Qy ValValHisGluLeuGluLeuTyrAsnThrGlyTyrLeuGlyMetPheMetAsnSer 629  
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Qy PheAlaValPheGlnGlyCysGlyLeuTyrValLeuThrAspAla----- 644  
Db GCCCGTGTCTTCCAGCAGCAGGCGCTGACCTTCACGAGCAGCAGTGGCCAGCAGACCGCC 2014  
Qy ----- 644  
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Qy -----AsnLeuThrLysAspTyrIle 651  
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QY 652 AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu 666  
Db 2135 GACGGCATCGGGAGAACCCCATGAGTTCTCGTGCACCGGGACCGCTTCATCTCC 2194  
QY 667 GluAsnGlu-----GlyHisIleValAspIleHis 676  
Db 2195 CTGGCGGAGCGGTGCAAGAGTCTTCCTGAGCTGTGCAATACATCAGAGCTCGCG 2254  
QY 677 -----AspPheSerLeu 680  
Db 2255 CGGCAGCAGCGCGGGCCACCCACTGGGCTGGCCAGGAGTAACCTGGATCAGGACATC 2314  
QY 681 GlySerSerProHisVal-----ArgLysHisPheProGluThrTrpIleTrp----- 696  
Db 2315 ATTGCAAGAGAACATCGTTTCCGAAAGTAGTTCCTCCAGAGAGTGGCTGTGGAACGT 2374  
QY 697 -----LeuAspThrAsnMetGlyTyrArgIleTyr 706  
Db 2375 GAGGACTTGAAGAGCCACCGAAATGGAATCTCTACGAGCTC----- 2419  
QY 707 GluGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal 726  
Db 2420 -----ATGAATATATTTTGAAGAGACTCCATCACCACGTGGGAGATTCTGGCTGTGAGC 2473  
QY 727 IleSerGluAspLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGln 746  
Db 2474 ATGTCGAGCAAGAAAGGATC-----TGTGGGAGACCCCTTCAGGTACAGTAATGCGAG 2530  
QY 747 ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu 766  
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QY 786 ---LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804  
Db 2648 CTCACATCCAGCTCTCGACCTTGCACCTGGCCACCAACAGAGG-----CGTCAC 2695  
QY 805 GluGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro 824  
Db 2696 CAGCAGACCAATAACATCCCGCCCAAGTCTCTGTTGCTCCATGTCTCATGTCGTGCGC 2755  
QY 825 -----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer 842  
Db 2756 CTAAGACCGGCTGCAAGGAGTGAAGTCAAGCTGCTCTACCATCATTTTCATCAGT 2815  
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Db 2816 GACGGTGTCAAGGAGTCCCTGAAGTGTGCTCCGAGAGGAATCAGAATGAACAAACTGTG 2875  
QY 863 SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu 880  
Db 2876 GCTGTT---CGCACCTTGGATCCCAAGACCGCTGGCGCGTGAAGAGTGCAGAAAGAG--- 2929  
QY 881 SerPheSerPheProAsnThrVal-----ThrGlySerGluArg 894  
Db 2930 -----GACATCCACCTGACACCTCAGTGAACCAAGTCCCGGACACCGAGTCTGAGACC 2983  
QY 895 -----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly--- 910  
Db 2984 AGAATTCCTCTGCAAGGAGACCCAGTGGCCAGATGACAGAGGATGCGCTCGACGCGAA 3043  
QY 911 ---LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe 929  
Db 3044 CGGCTGAAGACCTCATTTGACCCCTCGGGCTGGCGGGAACAGACATGATCGGCATG 3103  
QY 930 AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeu 949  
Db 3104 ACGCCACGGTTCATCGCTGTGCTTACCTACCTGATGAACCGAGCAGTGGGAGAGTTCCGC 3163  
QY 950 LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966

Db 3164 CTAGAGAACGGCAGGGGCGCTTGGAGCTCATCAAGAGGGGTACACCCAGCAGCTGCC 3223  
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QY 997 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006  
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QY 1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly----- 1041  
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QY 1074 -----PheLeuLysSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089  
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QY 1110 MetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpValSerSerGluSer 1129  
Db 3677 TTTCTGACC----- 3691  
QY 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146  
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QY 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165  
Db 3752 TATGCCCTCTTGCC---CTACTGCAGCTAAAGACTTGACTTTGTGCTCCCTCGCTCGT 3808  
QY 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185  
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QY 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204  
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QY 1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229  
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QY 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe 1249  
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Db 4108 AGATCAACTCACTGTATAATAA-----TTGACCTCAAGCTCAC 4146  
QY 1269 aVal-----LysGluAsnLysAspAspLeuAsnHisValAspLe 1282

Db 4147 CATAAACACGACCGGAAACAGAAAGAGCGCTCAGGATGCCCAAGAACACTATGATCCT 4206  
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 Db 4207 TGAGATCTGTACCAAGTACCGGGAGACACAGGATGCCACTATGTCTATATTGACATATC 4266  
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 Db 4267 CATATGACTGCTTGTCTCAGACACAGATGACCTGAGCAGCTGCCAATGGTGTGA 4326  
 QY 1317 rGluThrValLysLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332  
 Db 4327 CAGATACATCTCCAAAGTATGAGTGGACAAAGCCCTTCCGATAGGAACACCCCTCATCAT 4386  
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 QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371  
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 QY 1371 gArgGluAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388  
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 RESULT 8  
 US-09-142-334-23  
 ; Sequence 23, Application US/09142334  
 ; Patent No. 6268485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parries, Timothy C.  
 ; APPLICANT: Harrison, Richard A.  
 ; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase  
 ; FILE REFERENCE: 4-30443/A/INU/PCF  
 ; CURRENT APPLICATION NUMBER: US/09/142,334  
 ; CURRENT FILING DATE: 1999-04-15  
 ; EARLIER APPLICATION NUMBER: PCT/GB97/00603  
 ; EARLIER FILING DATE: 1997-03-04  
 ; NUMBER OF SEQ. ID NOS: 35  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 23  
 ; LENGTH: 5067  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-142-334-23  
 Alignment Scores:  
 Pred. No.: 1,2e-89 Length: 5067  
 Score: 931.00 Matches: 381  
 Percent Similarity: 40.88% Conservative: 287  
 Best Local Similarity: 23.32% Mismatches: 609  
 Query Match: 12.67% Indels: 358  
 DB: 3 Gaps: 63  
 US-10-020-095-4 (1-1428) x US-09-142-334-23 (1-5067)  
 QY 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22  
 Db 76 GGTCCAGCTGTG-----CTCCTGCTACTAACCCACCTCCCTCCCTGCTG 123  
 QY 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleIleArg----- 37  
 Db 124 GGG---AGTCCCATGTACTATCATCAACCCCAACATCTTGGCGTGGAGCGAGGAG 180  
 QY 38 -----ProGlyGlyAsnValThrIleGlyValGluLeuLeu 49  
 Db 181 ACCATGGTGTGAGGCCCAACGACGCGCAAGGGGATGTTCCAGTCACTGTTACTGTCCAC 240

QY 50 GluHis-----CysProSerGlnValThrValLysAlaGluLeuLeu 63  
 Db 241 GACTTCCCGAGCAAAAACACTAGTGTCTCCAGTGAGAAAGACTGTGCTGACCCCTGCCACC 300  
 QY 64 LysThrAlaSerAsnLeuThrValSerVal---LeuGluAlaGluGlyValPheGluLys 82  
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 QY 83 GlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyr 102  
 Db 361 GGGCGCAACAAGTTCTGACCGTGCAGGCC-----ACCTTCGGGACCCCAAGTGTG 411  
 QY 103 GluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeu 122  
 Db 412 GAGAAGGTGGTGTGGTGTGAGCTGAGCGCGGTACCTC----- 450  
 QY 123 SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro 142  
 Db 451 -----TTTCATCCAGACAGACAAAGACCATCTACACCCCT 483  
 QY 143 LysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThr 162  
 Db 484 GCCTCCACAGTTCCTATCGGATCTTACCCTCAACCAAGCTGCTACCGTGGCGCG 543  
 QY 163 SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGln---TrpLeuSer 181  
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 QY 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro 236  
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 QY 237 LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyr 256  
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 QY 257 GlyLysProValLysGlyAspValThrLeuThrPhe----- 268  
 Db 844 GGGAAAGAAAGTGGAGGAACTGCTTGTCTATCTTCGGGATCCAGGATGGGAACAGG 903  
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 QY 300 LysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGly 319  
 Db 1024 AAGTCTTTGTACGTGTCTGCC----- 1044  
 QY 320 ProValGluIleLeuThrValThrGluSerValThrGlyIleSerArgAsnValSer 339  
 Db 1045 -----ACCGTCACTTCGACTCAGGAGTGCATGTCAGGAGCGC 1089  
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Db	1210	GCCTACGAGTCCCGTGGCAGTCCAGGCGAGGACACTGTGCAGTCTCTAACCCAGGGA	1269
Qy	397	AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln	416
Db	1270	GATGGGTGGCCAACTCAGATCAACACACACCCAGCCAGGAG	1314
Qy	417	LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu	436
Db	1315	-----CCCTTGAGCATCAGCGTGGCAGCAAGAACAGGAGCTCTCG	1356
Qy	437	AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal	456
Db	1357	GAGGCGAGCAG-----GCTACGAGGACCATGAGGCTCTG	1392
Qy	457	HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr-----	472
Db	1393	CCCTACAGACCGTGGGCACTCAACAAATTACTGCACTCTCTCAGTGCTACGTACAGAG	1452
Qy	473	-----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn	490
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Qy	491	LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly	510
Db	1513	GCACAGATCCGCTACTACACTACCTACCTCATCTGATCAACAGGCGAGGCTGTGAGCGCGGA	1572
Qy	511	Lys-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSer	524
Db	1573	CGCCAGGTGCGAGAGCCGCGCAGGACCTGGTGGTGTGCTGCCCTGCCATCACACCGAC	1632
Qy	525	TrpThrProLysAlaCysValIleValTyr-----IleGluAspAspGly	540
Db	1633	TTATCCCTTCTTCGCGCTGGTGGGTACTACACGCTGATCGTGGCGGCGCAGAGG	1692
Qy	541	GluIleSerAspValLeuLysIleProValGln-----LeuVal	554
Db	1693	GAGTGGTGGCCGACTCCGNGTGGTGAGTCAAGACTCTCTGCTGGGCTCGCTGGTG	1752
Qy	555	PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu-----	569
Db	1753	GTAAAGCGCGC-----CAGTCAGAGACCGGCGCCTGTA	1788
Qy	570	ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle	589
Db	1789	CTTGGCGAGCAGATGACCTTGAGATAGAGGTGACACCGGCGCCGGTGGTA---CTG	1845
Qy	590	ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn	609
Db	1846	GTGCGCGTGACAAAGGCGGTCTGCTGCTGAATAAGAAAGAACAACTGACGCGAGTAAG	1905
Qy	610	ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer	629
Db	1906	ATCTGGGACGTGGTGGAGAGGCGACATCGCTGCAACCCCGGCGAGTGGGAAGGATTAC	1965
Qy	630	PheAlaValPheGlnGluCysGlyLeuTyrValLeuThrAspAla-----	644
Db	1966	GCCGCTCTCTCCGACGCGGCGTCACTTACAGGAGCAGCAGTGGCCAGCAGACCGCC	2025
Qy	644	-----	644
Db	2026	CAGAGGCGAGAACTTCAGTGCCTGCGCAGCAGCCCGCGCGCGTTCCTCGTCAGCTC	2085
Qy	645	-----AsnLeuThrLysAspTyrIle	651
Db	2086	ACGAGAGAGCGAATGGCAAGTCGGCAAGTACCCCAAGGAGCTGGCAAGTCTCGGAG	2145
Qy	652	AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu	666
Db	2146	GACGGCATCGGGAGAAACCCCATGAGTTCCTGTCGCCAGCGCGGACCCCGTTTCATCTCC	2205
Qy	667	GluAsnGlu-----GlyHisIleValAspIleHis	676

Db	2206	CTGGCGAGGCGTCAAGAGGTTCTTCTGGACTGTGCAACTACATCACAGAGCTGGG	2265
Qy	677	-----AspPheSerIleu	680
Db	2266	CGGCAGCACGCGCGGCGCAGCCACTGGGCTGTGCCAGGAGTAACCTGGATGAGACATC	2325
Qy	681	GlySerSerProHisIleVal-----ArgLysHisPheProGluThrTrpIleTrp	696
Db	2326	ATTGCAAGAGAATCTGTTTCCGGAAGTGTCCAGAGAGCTGTGCTGGAACTGT	2385
Qy	697	-----LeuAspThrAsnMetGlyTyrArgIleTyr	706
Db	2386	GAGGACTTTGAAGAGCCACCGAAAAATGGAATCTCTACGAAGCTC-----	2430
Qy	707	GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal	726
Db	2431	-----ATGAATATATATTTTGAAGAGACTCCATCCACCGTGGAGATTCTGGCTGTGAGC	2484
Qy	727	IleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPheGln	746
Db	2485	ATGTCGGCAAGAAAGGGATC---TGTGTGCACACCCCTTCGAGGTACAGATATGCGAG	2541
Qy	747	ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu	766
Db	2542	GACTTCTTTCATCGACTCGGCTACCTCTCTGTGTTTCCAAAACGACGAGGTGAAATC	2601
Qy	767	GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleGlu---	785
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Qy	786	---LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis	804
Db	2659	CTCCACATCCAGCCCTCTCGAGCTGGCCACCACCAAGAGG-----CGTCAC	2706
Qy	805	GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro	824
Db	2707	CAGCAGACATAAATC-----CAGGAGTCCCTGCTGCTCCGTTCATATGTCTATCGTCCG	2766
Qy	825	-----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer	842
Db	2767	CTAAGAGCGGCTCGCAGAGTGAAGTCAAGGTGCTGTCTACCATCAITTCATCATG	2826
Qy	843	AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln	862
Db	2827	GACGCTGTGAGAGTCCCTGAAAGTCTGTCGGAAGGAATCAGAATGAACAACTCTG	2886
Qy	863	SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu	880
Db	2887	GCTGTT---CGCACCTTGATCCAGAACGCTTGGCCCTGAAGAGTCCAGAAAGAG---	2940
Qy	881	SerPheSerPheProAsnThrVal-----ThrGlySerGluArg	894
Db	2941	-----GACATCCACCTGCAGACCTCAGTCAAGTCCCGGACACCGAGTCTGAGACC	2994
Qy	895	-----ValGlnIleThrAlaIleGlyaspValLeuGlyProSerIleasnGly---	910
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Qy	911	---LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe	929
Db	3055	CGGCTGAAGCACCTCATTTGTGACCCCTCGGGCTCGGGGAACAGACATGATCGCATG	3114
Qy	930	AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeu	949
Db	3115	ACGCCACCGTTCATCGTGTGCAATTACCTGGATGAACGGGACAGTGGGAGAGTTCGCG	3174
Qy	950	LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu	966
Db	3175	CTAGAGAGCGGCGAGGGGCTTTGAGGTCTATCAAGAGGGGTATACCCAGCAGCTGGCC	3234
Qy	967	TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr	986
Db	3235	TTACAGACACCCAGCTCTGCTTTCGGGCTTCGTGAAACCGGGCACCC-----AGCACC	3288

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QY 987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006
DB TGGTGTACCGCTACGTTGGTCAAGCTCTTCTCTGCTGTCAACCTCATCGGCATCGAC 3348
QY 1007 GlnAsnValLeuHisArgThrTyrThrTrpLeu---LysGlyHisGlnLysSerAsnGly 1025
DB TCCCAAGTCTCTCGGGGGCTGTTAAATAGCTGATCTCTGGAGAAGAGCCGACGGG 3408
QY 1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGly----- 1041
DB GTCTTTCAGGAGGATGCGCCGCTGATACACCAAGAAATGATGTTGGTATACGGAACAAC 3468
QY 1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061
DB AACGAGAAAGACATGGCCCTCAGCGCTTTGTTCTCATCTCGCTG----- 3513
QY 1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073
DB ---CAGGAGGCTAAAGATATTGCGAGGAGCAGGTCAACAGCTGCCAGGACGATCACT 3570
QY 1074 ---PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089
DB ---ATGAACCTACAGAGATCCTACACTGTG 3627
QY 1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109
DB GCCATTGCTGCTATGCTCTGGCCAGATGGCAGGCTGAGGGGCTCTTCTTAAACAA 3687
QY 1110 MetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrpValSerSerGluSer 1129
DB TTTCTTGACC-----ACAGCC 3702
QY 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146
DB AAAGATAGAACCCCTGGAGGACCTGTGTAAGAGCTCTACACGTGGAGGACCATCC 3762
QY 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165
DB TATGCCCTCTGGCC---CTACTGCAGCTAAAGACTTTGACTTTGTGCTCCGCTCGTG 3819
QY 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185
DB CGTTGGCTCAATGAACAGAGATACACTAGCTGGTGGCTATGCTCTACCCAGGCCCTTC 3879
QY 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204
DB ATGCTGTTCCAGGCTTGGCTCAATACCAAGAGAGCCCTGCACCACCAAGGAACGAAC 3939
QY 1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218
DB CTTGATGTGCTCTCCAACTGCCACCGC-CAGCTCAAGATACCCACCGATATCCACTG 3998
QY 1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229
DB GGAATCTGCAGCTCTCTGCTGATCAGAGAGACCAAGAGAAATGAGGGTTTCACATCAC 4058
QY 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe 1249
DB AGCTGAAGGAAAGGCCAAGGCCACTTGTGCGTGGTGACAACTTACCATGCTAAGGCCAA 4118
QY 1249 rGlySerSerArgArgArgSerIleGlnAsnGlnAlaPheAspLeuAspValAl 1269
DB AGATCAACTCACCTGTAATAA-----TTGACCTCAAGTCTAC 4157
QY 1269 aVal-----LysGluAsnLysAspAspLeuAsnHisValAspLe 1282
DB CATAAACACAGCAGCCGGAACAGAAAGAGCGCTCAGGATGCCAAGAACACTATGATCCT 4217
QY 1282 uAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValas 1302
DB TGATCTGTACCAAGGTACCAGGAGACCAAGGATGCCATATGCTATATATGACATATC 4277

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QY 1302 nLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317
DB CATGATGACTGCTTGTCTCCAGACACAGATGACCTGAAGCAGCTGGCCAAATGGTGTTGA 4337
QY 1317 rGluThrValLysLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332
DB CAGATACATCTCCAAGTATGAGCTGGACAAAGCCTTCTCCGATAGGAACACCTTCATCAT 4397
QY 1332 uTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValArgAs 1351
DB CTACCTGACCAAGGCTCTCACACTCTGAGGATGACTGTCTAGCTTTCAAGTTCACCAATA 4457
QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371
DB CTTTAAATGTAGAGCTTATCCAGCTGGAGCAGTCAAGGTCTACGCTATTACACCTTGA 4517
QY 1371 gArgGlnAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388
DB GGAAAGCTGTACCCGGTTTACCATTCCGAAAGAGGAGGATGGAAGCTGAACAAG----- 4572
QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401
DB ---CTCTGCCGTGAT---GAACTGTCGCTGTGCTGAGGAG 4608
RESULT 9
US-09-566-921-107
; Sequence 107, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 107
; LENGTH: 5129
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Incyte ID NO. 6682888 1000186.8
US-09-566-921-107
Alignment Scores:
Pred. No.: 1,58e-89 Length: 5129
Score: 930.00 Matches: 381
Percent Similarity: 40.88% Conservative: 287
Best Local Similarity: 23.32% Mismatches: 609
Query Match: 12.66% Indels: 358
DB: 4 Gaps: 63
US-10-020-095-4 (1-1428) x US-09-566-921-107 (1-5129)
QY 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22
DB 91 GGTCCACCGCTGTG-----CTCCTGTCTACTAACCCACCTCCCTCGCTCTG 138
QY 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleIleArg----- 37
DB 139 GGG---AGTCCCTGTACTCTATCATCACCCTCCCACTCTGCGCTGGAGCGAGGAG 195
QY 38 -----ProGlyGlyAsnValThrIleGlyValGluLeu 49
DB 196 ACCATGGTGTGGAGGCCGCCAGCGCGCAAGGGGATGTTCCAGTCACTGTATTCTGCCAC 255
QY 50 GluHis-----CysProSerGlnValThrValLysAlaGluLeu 63
DB 256 GACTTCCCGCGCAAAAAAAGCTAGTGTCTGTCCAGTGAGAGACTGTGTGACCCCTGCCACC 315

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QY 64 LysThrAlaSerAsnLeuThrValSerVal---LeuGluAlaGluGlyValPheGluLys 82  
Db 316 AACACATGGCAACGTCACCTTCAGATCCCAAGCAAGAGGAGTCAAGTCAGAAAG 375  
QY 83 GlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluLeuTyr 102  
Db 376 GGGCGCAACAGTTCGTGACCGTGCAGGCC-----ACCTTCGGGACCCCAAGTGGTG 426  
QY 103 GluLeuArgValThrGlyArgThrGlnAspGluLeuPheSerAsnSerThrArgLeu 122  
Db 427 GAGAAGGTGTGTGTGTCACCCCTGCAGAGCGGTACCTC----- 465  
QY 123 SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro 142  
Db 466 -----TTCATCCAGACACAGACCACATCTACACCCCT 498  
QY 143 LysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThr 162  
Db 499 GGCTCCACAGTCTCTATCGATCTTCACCGTCAACCAAGCTGTACCCGTGGCGCG 558  
QY 163 SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGln---TrpLeuSer 181  
Db 559 ACGETCATGTCAACATGAGAACCCGGAAGGCATCCCGTCAAGCAGGACTCTCTGTCT 618  
QY 182 GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeu 201  
Db 619 TCTCAGAACCAAGCTTGGCGTCTTGGGACATTCCGGAACCTCGTCAACATG 678  
QY 202 GlyAspTrpSerIleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSer 218  
Db 679 GGCAGTGGGAAGTCCGAGCCTACTATGAATCAACCAAGAGGCTCTCCACTGAG 738  
QY 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro 236  
Db 739 TTTGAGTGAAGAGTACGTCTGCCAGTTTCGAGTTCATAGTGCATAGTGGAGCTACAGAGAA 798  
QY 237 LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyr 256  
Db 799 TTCTACTACATCTATACGAGAAGGCGCTGGAGTCAACATCACCAGGCTCTCTAC 858  
QY 257 GlyLysProValLysGlyAspValThrLeuThrPhe----- 268  
Db 859 GGAAGAAGTGGAGGAAGTGGCTTTGTCTCTTCGGATCAGAGTGGCGAACAGAGG 918  
QY 269 -----LeuProLeuSerPheTrpGlyLysLysLysAsn 279  
Db 919 ATTTCCCTGCCTGAATCCCTCAAGCGCATTCAGATTGAGGATGGCTCGGGGAGGTGTG 978  
QY 280 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMet 299  
Db 979 CTGAGCCGGAAGTACTGCTGGACGGGGTGCAGAACCCCGAGACAGAACCTGTGGGG 1038  
QY 300 LysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGly 319  
Db 1039 AAGTCTTTGTACGTGCTGCC----- 1059  
QY 320 ProValGluLeuLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSer 339  
Db 1060 -----ACCGTCATCTTGCATCAGGCGATGACATGTGTGAGGAGAGCGC 1104  
QY 340 ThrAsnValPhePheLysGlnHisAspTyrIleLeuPhePheAspTyrThrThrVal 359  
Db 1105 AGCGGATCCCATCGTGACCTCTCCCTACAGATCCATTCACCAAGACACCCCAAGTAC 1164  
QY 360 LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn--- 378  
Db 1165 TTCAACACCAAGATGCCCTTTGACCTCATGTGTCTGTGACGAACCTGTATGCTCTCCA 1224  
QY 379 -----GlnLeuThrLeuGluArgArgAsnValValIleThrValThrGlnArg 396  
Db 1225 GCCTACCGAGTCCCGTGGCAGTCCAGGGGAGGACACTGTGAGTCTCTAACCCAGGGA 1284  
QY 397 AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln 416

Db 1285 GATGCGTGGCCAAACTCAGCATCAACACACCCCAAG----- 1329  
QY 417 LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu 436  
Db 1330 -----CCCTTGAGCATCAGGTGCGCAGGAAGACAGAGCTCTCG 1371  
QY 437 AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal 456  
Db 1372 GAGGAGAGCAG-----GCTACGAGCACCATGAGGCTCTG 1407  
QY 457 HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr----- 472  
Db 1408 CCTACAGCACCGTGGGCAACTCCAAACAATTACCTGTCATCTCTCAGTCTAGTACAGAG 1467  
QY 473 -----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn 490  
Db 1468 CTCAGACCCGGGAGACCCCTCAACGTCAACTCTCTGCAATGGACCGGCCACAG 1527  
QY 491 LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510  
Db 1528 GCCAAGATCCGCTACTACACTCTGATCATGAACAGGCGAGCTGTGAGCGGGA 1587  
QY 511 Lys-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSer 524  
Db 1588 CGCCAGGTCCGAGACCCCGGCGAGACCTGGTGTGTCTGCCCCCTGTCATCACCACCGAC 1647  
QY 525 TrpThrProLysAlaCysValIleValTyr-----IleGluAspAspGly 540  
Db 1648 TTCTATCCCTTCTCCGCTGTGTGCTGCTACTACGCTGTCGTCGCGCCAGCGCCAGAGG 1707  
QY 541 GluIleIleSerAspValLeuLysIleProValGln-----LeuVal 554  
Db 1708 GAGTGTGTGGCGACTCCGTGTGGTGCAGCTCAAGGACTCTCTGCTGGTGGTCTGCTGTG 1767  
QY 555 PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu----- 569  
Db 1768 GTAAAAACCGC-----CAGTCAGAACACCGGCGAGCTCTGA 1803  
QY 570 ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle 589  
Db 1804 CTGCGGAGCAGATACCTCTGAAGTAGAGGTGACACCGGGCCCGGGTGTGTA---CTG 1860  
QY 590 ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn 609  
Db 1861 GTGGCGTGGACAAGGGCGTGTCTGTCTGAATAAGAAACAACAACTGACACAGAGTAAG 1920  
QY 610 ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer 629  
Db 1921 ATCTGGGAGTGTGTGGAAGAGCAGACATCGCTGACCCCGGCGAGTGGGAGGATTAC 1980  
QY 630 PheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAla----- 644  
Db 1981 GCCGTGTCTTCTCCGACGACGGGTGACCTTCAGAGCAGCAGTGGCGCAGACCGCC 2040  
QY 644 ----- 644  
Db 2041 CAGAGGGCAGAACTTTCAGTGGCCGAGCAGCGCCCGCCGAGCGCTTCGCTGAGCTC 2100  
QY 645 -----AsnLeuThrLysAspTyrIle 651  
Db 2101 ACGGAGAGCGAATGGACAAGTCGGCAAGTACCCCAAGGAGCTGCGCAGTGTGTCGAG 2160  
QY 652 AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu 666  
Db 2161 GACGCGTGGGAGAACCCCATGAGGTCTCTGTCGACCGCGGACCGCTTTCATCTCC 2220  
QY 667 GluAsnGlu-----GlyHisIleValAspIleHis 676  
Db 2221 CTGGCGAGGGGTGCAAGAGGTCTTCTGAGTCTCTCAACTACATCAGAGAGTGGCG 2280  
QY 677 -----AspPheSerLeu 680  
Db 677 -----

Db 2281 CGGCAGCACGGCGGGCCAGCCACCTGGCGCTGCCAGGAGTAACCTGGATGAGGACATC 2340  
Qy 681 GlySerSerProHisVal-----ArgLysHisPheProGluThrTrpLeu----- 696  
Db 2341 ATTCGAGAGAACATCGTTTCCGGAAGTAGGTTCCAGAGAGCTGGCTGGGAGGTT 2400  
Qy 697 -----LeuAspThrAsnMetGlyTyraArgIleTyr 706  
Db 2401 GAGGACTTGAAGAGCCACCGAAATGGAATCTCTACGAAGCTC----- 2445  
Qy 707 GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal 726  
Db 2446 -----ATGAATATATTTTGAAGACTCCATCACACGCGGAGATCTGGCGTGCAGC 2499  
Qy 727 IleSerGluAspLeuGlyLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGln 746  
Db 2500 ATGTGCGCAAGAAAGGATC---TGTTGGCAGACCCCTTCGAGGTTCACAGTAATGCAG 2556  
Qy 747 ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu 766  
Db 2557 GACTTCTTCATCGACTCGCGCTACCTCTCTGTTCGAAACGAGCAGGTGCGAAATC 2616  
Qy 767 GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu--- 785  
Db 2617 CGACCGCTCTCTACAAATTAC---CGGCAGAACCAAGAGCTCAAGGTGAGGGTGAAC 2673  
Qy 786 ---LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804  
Db 2674 CTCACAAATCCAGCTTCTGAGCTGGCCACCAAGAGG-----CGTCAAC 2721  
Qy 805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro 824  
Db 2722 CAGCAGACCGTAACCATCCCGCCCAAGCTCTGTTGTCCTTCCATATGTCATCGTGGCG 2781  
Qy 825 -----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer 842  
Db 2782 CTAAAGACCGCGCTGCAGGAAGTGAAGTCAAGCTGCGCTCTACCATCATTTTCATCAGT 2841  
Qy 843 AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln 862  
Db 2842 GACCGTGTCAAGAAATCCCTGAAGTCTGCTGCCGGAAGGAATCAGAAATGAACAAACTGTG 2901  
Qy 863 SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu 880  
Db 2902 GCTGTT---CGCACCTGGATCCAGAACGCTGCGCGCTGAGAGTGCAGAAAGAG--- 2955  
Qy 881 SerPheSerPheProAsnThrVal-----ThrGlySerGluArg 894  
Db 2956 -----GACATCCACCTGCAGACCTCAGTGCACCAAGTCCCGGACACCGAGTCTGAGAC 3009  
Qy 895 -----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly--- 910  
Db 3010 AGAATTCCTCGCAAGGACCCCGAGTGGCCAGATGACAGAGGATCGCTGCGACGGAA 3069  
Qy 911 ---LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe 929  
Db 3070 CGGCTGAAGCACCTCAITGTGACCCCTCGGCTGCGGGGACAGAACATGATCGGCATG 3129  
Qy 930 AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeu 949  
Db 3130 ACGCCCAAGGTTCATCGCTGTGCATTACTGTGATGAACGAGGAGGATGGGAGAGTTCGGC 3189  
Qy 950 LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966  
Db 3190 CTAGAGAAGCGGACGGGCGCTTGAGCTCATCAAGAAGGGGTACACCCAGCAGCTGGCC 3249  
Qy 967 TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986  
Db 3250 TTCAGACAAACCCAGCTCTGCTTGGCGCTCTGCTGAAACGCGGCACCC-----AGCAC 3303  
Qy 987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006  
Db 3304 TGGCTGACCGCTACGTGGTCAAGGTTCTTCTCTGCTCTCAACCTCATCGCCATCGAC 3363

Qy 1007 GlnAsnValLeuHisArgThrTyrThrTrpLeu---LysGlyHisGlnLysSerAsnGly 1025  
Db 3364 TCCCAAGTCTCTCGGGGCTGTTAAATGGCTGATCTGGAGAAAGACAGACCGACGG 3423  
Qy 1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly----- 1041  
Db 3424 GTCTTCCAGGAGGATCGCCCTGTATACACCAAAATGATGTGTGATTCAGGAACAAC 3483  
Qy 1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061  
Db 3484 AACGAGAAAGACATGGCCCTCACGSCCTTGTCTCATCTCGCTG----- 3528  
Qy 1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073  
Db 3529 ---CAGGAGGCTAAGATATTTGCGAGGAGCAGGTCAACAGCCTGCCAGGAGCATCACT 3585  
Qy 1074 -----PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089  
Db 3586 AAAGCAGGAGACTTCTTGAAGCCAACTAC---ATGAACCTACAGAGATCCTACACTGTG 3642  
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Qy 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146  
Db 3718 AAAGATAGAACCTGCGAGGACCTCGTAAGCAGCTCTACACAGTGGAGGCCACATCC 3777  
Qy 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165  
Db 3778 TATGCTCTCTTGGCC---CTACTGCGCTAAAAGACTTTTGACTTTGCTCCCTCGTGTG 3834  
Qy 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyPheAlaSerThrGlnAspThrThr 1185  
Db 3835 CGTTGGCTCANTGACAGAGATACACGGTGGTGGCTATGGCTCTACCCAGGCCACCTTC 3894  
Qy 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204  
Db 3895 ATGGTGTTCGAAGCTTGGCTCAATACCAAAAGAGCGCCCTGACCCAGGAACTGAAC 3954  
Qy 1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218  
Db 3955 CTGTATGTGCTCCCTCAACTGCCAGCGG-CAGCTCCAGATCACCCACCGTATCCACTG 4013  
Qy 1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229  
Db 4014 GGAATCTCCAGCTCTCTCGATCAGAAGAGACCAAGAAATGAGGGTTTCACAGTCAC 4073  
Qy 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe 1249  
Db 4074 AGCTGAAGAAAGGCCCAAGGCACCTTGTGCTGGTGGACATGTACCATGTAAAGGCAA 4133  
Qy 1249 rGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAl 1269  
Db 4134 AGATCAACTCACCTCTAATAA-----TTGACCTCAAGGTCAAC 4172  
Qy 1269 aVal-----LysGluAsnLysAspAspLeuAsnHisValAspLe 1282  
Db 4173 CATAAACCCAGCAGCCGGAACACAGAAAGAGCCCTCAGGATGCCAAGAACACTATGATCCT 4232  
Qy 1282 uAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAs 1302  
Db 4233 TGAGATCTGTACCAAGTACCGGGAGACCGAGTGCACATGTATGTATATTTGGACATATC 4292  
Qy 1302 rLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317  
Db 4293 CATGATGACTGGCTTGTCTCCAGACACAGATGACCTGAAGCAGCTGGCCCAATGTTGTGA 4352

QY 1317 rGluThrValIysLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332  
Db 4353 CAGATACATCTCCAAAGATGAGTGGACAAAGCTTCTCCGATAGGAAACACCCCTCATCAT 4412  
QY 1332 uTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValargas 1351  
Db 4413 CTACCTGGACAAGGTCACACTCTGAGGATGACTGCTAGCTTTCAAAGTTCACCAATA 4472  
QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371  
Db 4473 CTTTAATGTAGAGCTTATCCAGCTGGAGCAGTCAAGGTCCTACGCTATTACAACTGGA 4532  
QY 1371 gArgGlnAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388  
Db 4533 GGAAGCTGTACCGGTTCTACCATCGGAAAGAGGAGTGAAGAGCTGAACAAG----- 4587  
QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401  
Db 4588 -CTCTGCGGTGAT--GAAGTGTGCGCTGTGTGAGGAG 4623

## RESULT 10

US-08-662-227-1  
; Sequence 1, Application US/0866227  
; Patent No. 5922320  
; GENERAL INFORMATION:  
; APPLICANT: VOGEL, CARL-WILHELM  
; APPLICANT: BREDEHORST, REINHORST  
; APPLICANT: KOCK, MICHAEL  
; APPLICANT: FRITZINGER, DAVID  
; TITLE OF INVENTION: RECOMBINANT PROCVF  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C. JEFFERSON DAVIS HIGHWAY  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/662,227  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-0107-0X  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-662-227-1  
  
Alignment Scores:  
Pred. No.: 1,66e-85 Length: 5948  
Score: 894.00 Matches: 361  
Percent Similarity: 40.90% Conservative: 295  
Best Local Similarity: 22.51% Mismatches: 672  
Query Match: 12.17% Indels: 276  
DB: 2 Gaps: 56

US-10-020-095-4 (1-1428) x US-08-662-227-1 (1-5948)

QY 18 AlaAlaLeuAlaVal-----AlaProGlyProArgPheLeuValThrAla 32  
Db 31 GTGTCTTATTGATTTGGTTTCCAGGCTTCTCATGGGCTCTCTACACCTCATCACC 90  
QY 33 ProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis 51  
Db 91 CTGTCTGTTTTCGGAACAGACACAGAGAGCAAAATTTTGTGTGGAGCCCATGGAGACAGT 150  
QY 52 CysProSerGlnValThrValIysAla-----GluLeuLeuIleAlaSer 67  
Db 151 ACTCCAAACACAGCTTCACATCTTGTTCATGATTTTCACGGAAGCAGAAACCTTGTTC 210  
QY 68 AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr 87  
Db 211 CAAACAGAGATAGATGATGAATCCAGCAGGAGCATGCTTGTCACT-----CCAAC 261  
QY 88 LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThr 107  
Db 262 ATAGAGATTCCAGCAAAAGAGTGGATGAGTACGCACTCCAGGCAAAATCAATATGTGTGTG 321  
QY 108 GlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLys 127  
Db 322 CAAAGTAAGTGTCTCAAGTGAGATGGAAAAGGTGGTTCTCTTCTTACCAGAGTAGC 381  
QY 128 ArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys 147  
Db 382 -----TTCTGTGTTTATCCAGACAGATAAAGGCATCTATACACCGGGTCTCCAGTACTC 435  
QY 148 PheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu 167  
Db 436 TATCGTGTGTTTCTATGGATCACAACACAGCAGAGATGAACAAACCTGATGTTGTGAG 495  
QY 168 IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnGlnSerAspLeuGly 187  
Db 496 TTTCAGACTCCAGAAGGCATCTTGTCACT-----TCTAATTCAGTTGACCTAAAC 546  
QY 188 ValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTyrSerIle--- 206  
Db 547 TCTTTC---TGGCCTTACAATTTACCAGACCTGTGTGAGTTTGGGAGCTTGGAGGATGTG 603  
QY 207 ---GlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGluTyrVal 225  
Db 604 GCCAAATATGAACATTCGCCAGAGAAATATATCTCATATTTTGTATGTCAGGAATATGTG 663  
QY 226 LeuProLysPheGluValThrLeuGlnThrPro-----LeuTyrCysSerMetAsn 242  
Db 664 TTGCCAAGCTTTGAAGTCCGTCCTCAACCATCAGAGAAGTTTTTTTACATTGACGGCAAT 723  
QY 243 SerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGly 262  
Db 724 ---GAAATTTCCAGGTGCTCTCTCTGCAAGGTACTTGTATGAGGAGGAAGTGAAGGT 780  
QY 263 AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnIle----- 280  
Db 781 ---GTGGCCTTTGTCTCTCTTTGGAGTGAATAAGATGATGCTAATAAAGAGATTATCCAGAC 837  
QY 281 -----ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGlu 298  
Db 838 TCATCAGAGAATTCGATTATTGATGGAGATGGGAAAGCAACACTAAAGAGATACATA 897  
QY 299 MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro 318  
Db 898 TTCCGTTCTCGATTTCCAAAATCTCAATGAGCTTGTGGGCATCTCTGTATGATCATCT--- 954  
QY 319 GlyProValGluIleLeuThrValThrGluSerValThrGlyIleSerArgAsnVal 338  
Db 955 -----GTAACAGTTCATCAGCAAGATTCAGCGAGTGTATGTTAGTACTGAG 999  
QY 339 SerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThr 358  
Db 1000 CAAAGCGGCATTCATATTGTGGCATCTCCCTATCAGATCCACTTCACAAAAACCCCAAA 1059



Db 3106 GGTATGCCAGCAGATGGTGTACAGAAAGCAGATCATTCTTCATGCGCATTTTACAAAC 3165  
QY 980 TyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPhe---LeuGlu 998  
Db 3166 -----CGTCGATCTAGTCTTGGCTAACAGCATATGCTGTAAGAGCTTTGGCATGGCT 3219  
QY 999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu--- 1017  
Db 3220 GCCAAATAGTAGCAGCATATGATCATGAATCATTTGTGGAGGTGTGAGGTGGCTGATT 3279  
QY 1018 LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 1037  
Db 3280 CTGAACAGGCAACACACAGATGAGCGTTCAAGAAATGCCCTGTACTTCTTGAACA 3339  
QY 1038 LeuGlnGly-----GlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054  
Db 3340 ATGAGGAGGCAATTCAGGTGCTGAAGAGAGATATTTAAACAGCTTCAATCTGTT 3399  
QY 1055 SerLeuLeuGlyTyrArg-----LysTyrGlnProAsnIleAsp-----Val 1068  
Db 3400 GCCTTTGTGAATCCAAACAATCTGCAATGACTATGTCATTAATGCTAGACAGCAGCATC 3459  
QY 1069 GlnGluSerIlePheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088  
Db 3460 AAGAAGGCCCAAAATATTACTCAAAAAGATAGAGAA---CTGCAAGGCCCTTACACT 3516  
QY 1089 LeuAlaLeuLeuThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeu 1108  
Db 3517 ACAGCCCTCACAGCCATGCTTTGGCT-----GCTCAGACCAACATC 3558  
QY 1109 AsnMetLeuThrTrpArgAlaGluGlnGluGlyMetGlnPheTrpValSerGlu 1128  
Db 3559 AATGATCAGAGGTACTCTGCGAGCATCAACAGGAGGATCATTTG----- 3606  
QY 1129 SerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAla 1148  
Db 3607 -----GAAGAATACATGCTCACCCCAACATTTGAAGGCCACTTCTCTATGCC 3654  
QY 1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168  
Db 3655 TTGTTGGCCCTGCTGAAATGAAGAATTTGATCAAACTGGTCCCATAGTCAGATGGCTG 3714  
QY 1169 SerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeu 1188  
Db 3715 ACAGATCAGAAATTTTATGGGAAACATATGGACAAACCAACAGCAACATTTGGCATTT 3774  
QY 1189 LysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArg---ThrAsnIleGlnVal 1207  
Db 3775 CAAGCTCTTGCTGAATAGATTCAGATGCCTACCCTAACGACCTTAAACTTAGATATT 3834  
QY 1208 ThrValThrGlyProSerSerProSerProLeu----- 1218  
Db 3835 ACTATTGAAGTCCGATCGAGNAGTACCTTAAGGTACAGATTAATTAATAAATGCT 3894  
QY 1219 -----AlaValValGlnPro-----MetAlaValAsnIleSerAlaAsnGly 1232  
Db 3895 CTCCTGGCTCGGACAGTAGAGCAACCAACCAAGACATCACGTGACAGCATCAGT 3954  
QY 1233 PheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSer 1252  
Db 3955 GATGGAAGACCAATAGCAATTTTGGACATTTCTAATACGCACAGTGT----- 4002  
QY 1253 ArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGlu 1272  
Db 4003 CAGGAGAAGGCAATGTTTGAATAAA-----TTTCATCTTAATGTTTCTGTGAA--- 4053  
QY 1273 AsnLysAspAspLeuAsnHisValAsp-----LeuAsnValCysThr 1286  
Db 4054 ---AACATCCACTGTAATCAATGGAGCAAGGAGCCCTCATGCTCAAGATCTGCACA 4110  
QY 1287 SerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGly 1306  
Db 4111 AGGTATCTGGAGAACTTCAATCTACAAATGACAAATTAATTTCTATGCTGCTGCT 4170

QY 1307 PheMetValProSerGluAlaIleSer-----LeuSerGluThrValLys 1321  
Db 4171 TTTCCTCCCTGATGCTGAGACCTTACAGGCTTCTAAGAGGTGACAGATACATCTCC 4230  
QY 1322 LysValGluTyrAspHisGlyLysLeuAsn-----LeuTyrLeuAspSer 1336  
Db 4231 AGATATGAAGTTGACAATAATATGCTCAGAAAGTAGCTGTTATCATTTACTTAAACAAG 4290  
QY 1337 ValAsnGluThrGln---PheCysValAsnIleProAlaValArgAsnPheLysValSer 1355  
Db 4291 GTCTCCCACTCTGAAGATGAATGCTGCACCTTAAGATTCACAGCATTTGAAGTTGGC 4350  
QY 1356 AsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgGlnAlaVal 1375  
Db 4351 TTCATTGACGACGAGTACGTCAAGGTGTACAGCTACTACAATCTAGATGAATAATGTACC 4410  
QY 1376 ArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspValGlnGly 1395  
Db 4411 AAGTTCTACCATCCAGATAAAGGACAGGCGCTTCTCAATAAGATATGATTGGTAACGTT 4470  
QY 1396 CysArgProCysGluAspGlyAlaSerGlySerHisHis----- 1408  
Db 4471 TGCCGATGTGCAGGAGAAACCTGTTCTCGCTCAACCATCAGAAAGGATTTGATGTTCCA 4530  
QY 1409 -----HisSerSerValIlePhePheCysPheLysLeuLeu 1421  
Db 4531 TTACAAATTTGAAAAGCCTCGCAGACGAATGTGGATTATGTCTACAAACCAAGTGCTT 4590  
QY 1422 TyrPheMetGlu 1425  
Db 4591 CGAATAGAGAA 4602

## RESULT 11

US-09-017-947-1  
; Sequence 1, Application US/09017947  
; Patent No. 6303754  
; GENERAL INFORMATION:  
; APPLICANT: VOGEL, CARL-WILHELM  
; APPLICANT: BREDEHORST, REINHORST  
; APPLICANT: KOCK, MICHAEL  
; APPLICANT: FRITZINGER, DAVID  
; TITLE OF INVENTION: RECOMBINANT PROCVF  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,947  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/662,227  
; FILING DATE: 14-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/POCKET NUMBER: 1126-0107-0X  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

281	Qy	-----ThrIysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnApsGlu	298
838	Db	TCACTCCAGGAATCCGATTTATGTAGAGATGGGAAGCAACATAAAGAGATACA	897
299	Qy	MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro	318
898	Db	TTCCGTTCTCGATTTCCAAATCTCAATGAGCTTTGTTGGGCATCTCTGTATGATCT	954
319	Qy	GlyProValGluIleLeuThrValThrGluSerValThrGlyIleSerArgAsnVal	338
955	Db	-----GTAAACAGTCATGACAGAATCAGCGAGTGAATGGTAGTCACTGAG	999
339	Qy	SerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThr	358
1000	Db	CAAAAGGGCATTCATATTGTTGGCATCTCCCTATCAGATCCATTCACAAAACCC	1059
359	Qy	ValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn	378
1060	Db	TATTTCAAGCCAGGAATGCCATTAAGTAACATGACGGTGTATGTTACCAACCC	1119
379	Qy	GlnLeuThrLeuGluGluArgAsnAsnValIleIleThrValThrGlnAspAsnTyr	398
1120	Db	CCAGCT-----GCCATGTGCCATGGTATCAGAGGCCTTT	1155
399	Qy	ThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIle	418
1156	Db	-----CATTCTATCGGAACCACTTTTGATGATGGAGCTGTGAAGCTC	1197
419	Qy	AsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSer	438
1198	Db	ATCCTGAACATCACTGATGATGCTCAA-----AGCTACCAATCACTGTAGAACT	1248
439	Qy	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer	458
1249	Db	AACATGGAGACCTCCCAAGAGAAGCCAGGCAACAAAGTCCATGACAGCATAGCCTAC	1308
459	Qy	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478
1309	Db	CAAAACCCAGGAGGATCTGGAACACTATCTTCATGTAGCCATTACATCTACAGAGATTAA	1368
479	Qy	ValGlySer-----ProPheGluLeuValValSerGlyAsn-----LysArg	492
1369	Db	CCCGAGATAACTTACTGTCAATTCATGTGAAGGCCAATGCCAATTCACCTGAACGAG	1428
493	Qy	LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLys---	511
1429	Db	ATCAAAATATTTCATACCTCATCTGAAATAAAGGAAGATTTTTCAAAGTTGGCAGCAA	1488
512	Qy	-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSerTyrThr	526
1489	Db	CCCAGGAGATGGCGAATCTGTTGACCATGAATCTGCATATCACTCCAGATCTCATC	1548
527	Qy	ProLysAlaCysValIleValTyrTyrIleGluAspAspGlyGluIleIleSerAspVal	546
1549	Db	CCITCTCCGTTTGGGCTTACTACCAAGTGGGAACCAAGAAATTTGGTGTGATCTCT	1608
547	Qy	LeuLysIleProValGln-----LeuValPheLys-----AsnLys	558
1609	Db	GTCTGGGTGGATGTGAAGGATACCTGTCATGGGAACGTTGTTGTGAAGGAGACAATCTA	1668
559	Qy	IleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgile	578
1669	Db	ATCAAAATG-----CCAGGAGCTGCAATCAAAATGCAAAATTG	1704
579	Qy	SerValThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeu	598
1705	Db	GAA---GGGGATCCAGGTGCTCGGGTTGGTCTTGTGCTGTGGCAAGCAGATATATGTT	1761
599	Qy	MetAsnAlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsn	618
1762	Db	CTCAATGATAAATAAGATTAGTCCAGCTAAGATATGGGACACAATAGAAAGAGTGCAC	1821
619	Qy	ThrGlyTyrThrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeu	638

Db 1822 TTTGGCTGTACAGTGGCAGTCCAGATAAATCTGGGTGTGTTGAAGATGCTGGACTG 1881  
QY 639 TrpValLeuThrAspAlaAsnLeu-----ThrLysAsp----- 649  
Db 1882 GCTCTGACCAACCGACACTAATCTCAACACCAACAGAGATCAGCTGCAAAAGTGCTCTCAG 1941  
QY 649 ----- 649  
Db 1942 CTGCGAATCGGAGGCGTCCAGTCTCTGTTTCTGCTTGACAGCAACGCAAGCAAGCG 2001  
QY 649 ----- 649  
Db 2002 GCAGAAATTCAGGATCAAGACCTCGGTAAATGCTGTGAAGATGTCATGATGAGAACCC 2061  
QY 649 ----- 649  
Db 2062 ATGGGGTACCTGTGGAAGCGTGCAGAAATACATCCAGAGGAGATGCTTGTAAAGCT 2121  
QY 650 -----TyrIleAspGlyValTyAsp---AsnAlaGluTyAla 661  
Db 2122 GCCTTCTTGAATGCTGCTACATCAAGGGGTCGAGATGAARACCAACCGGAGAGC 2181  
QY 662 GluArgPheMet-----GluGluAsnGlu---GlyHisIleValAspIleHisaspPhe 678  
Db 2182 GAGTTGTTCTGCGCAAGAGATGATAATGAAGATGTTTCATGACGATAGTGATATCATC 2241  
QY 679 SerLeuGlySerProHisValArgLysHisPheProGluThrTrpIleLeu--- 697  
Db 2242 TCA-----AGTCTGATTTCCCAAGATGGTGGCTGATGCTTTCAT 2280  
QY 698 -----AspThrAsnMetGlyTyArgIleTyGlnGluPheGluValThr 712  
Db 2281 AAGGACTTGACCGAGGAGCTTAACAGTCAAGGGATTTCAGCAAGACAGATGCTTTTAT 2340  
QY 713 ValProAsnSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly 732  
Db 2341 CTGAGGATTCATCAACACCTGGTGGTGGCTGATGAGTTTACACCCACCAAGGG 2400  
QY 733 LeuGlyLeuThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu 752  
Db 2401 ATC---TGTTGGCTGAACCTTATGAATAAGAGTCATGAAGTCTTCTTCATGATCTT 2457  
QY 753 AsnLeuProTySerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn 772  
Db 2458 CAAATCCCATATTCAGTAGTGAAGATGACGAGGTGGAGATTCGAGCTATTCTGCACAA 2517  
QY 773 TyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAspIle 792  
Db 2518 TAGTTTAAACGAGATATTTATGTCGAGTGGACTGTGTTATACACCCAGCTTC 2571  
QY 793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812  
Db 2572 -----TGCAAGTCTTCCCAAAAGGACAAAGATACCGACAGTTCCTCAATTAAGCC 2625  
QY 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly-----GluIle 830  
Db 2626 CTGTCCTCCAGACGATACCGTTTGATGAGTCCCATTAAGCAAGGATTCATGATGTT 2685  
QY 831 ProIleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu 850  
Db 2686 GAGATTAAGCAAGTCTCCAGGAAGCGTTGTCGTCAGACGGTGTGAGGAGAACTGAAA 2745  
QY 851 ValLysAlaGluGlyIleGluLysSerTySerGlnSerIleLeuLeuAspLeuThrAsp 870  
Db 2746 GTTGTACCTGAAGGGGTACAGAAATCCATTGCTGACTATTGTTAAACTGGACCAAGGCA 2805  
QY 871 AsnArgLeuGlnSerThr-----LeuLysThrLeuSerPhePhe 884  
Db 2806 AAGAGGTGGTGGACACAGCTAGAGTGATCAAGCCCGCAAAATTCATGACAGAGTG 2865  
QY 885 ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu 904  
Db -----

Db 2866 CCTGCACAGAAATGAACCAAGATTATCATCCAGGTGACCCTGTGGCTCAGATTATT 2925  
QY 905 GlyProSerIleAsnGly-----LeuAlaSerLeuIleArgMetProTyArgCysGly 922  
Db 2926 GAAAACTCAATTGATGGAAGTAAACTCAACCATCTCTATTATCACTCTCTGTGGTGTGG 2985  
QY 923 GluGlnAsnMetIleAsnPheAlaProAsnIle-----TyrIleLeuAspTyLeu 939  
Db 2986 GAGCAAAATATGATCCGATCGCCGACCAAGTATTATGCCACTACTACTCGACACCAACA 3045  
QY 940 ThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGln 959  
Db 3046 GAGCAGTGGGAGACTCTCGGCATAAATCGCAGACTGAAGCTGTCAATCAGATCGTGACT 3105  
QY 960 GlyTyArgGluLeuLeuTyGlnArgGluAspGlySerPheSerAlaPheGlyAsn 979  
Db 3106 GGTATGCCCCAGAGATGGTGTCAAGAAAGCAGATCATCTCTATGACGACTTACAAAC 3165  
QY 980 TyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPhe---LeuGlu 998  
Db 3166 -----CCTGCATCTAGTCTTGGCTAACACGATATGCTGAAAGCTTTGCCATGGCT 3219  
QY 999 AlaAspProTyIleAspIleAspGlnAsnValLeuHisArgThrTyThrTrpLeu--- 1017  
Db 3220 GCCAAATGTTAGCAGGCAATTAGTCATCAATCATCTTGTGAGGTGTGAGGTGGCTGATT 3279  
QY 1018 LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 1037  
Db 3280 CTGAACAGGCAACCAACGATGGAGCGTTCAAGAAATGCCCTGTACTTCTTCTGGAACA 3339  
QY 1038 LeuGlnGly-----GlyAsnLysSerProValThrLeuThrAlaTyIleValThr 1054  
Db 3340 ATGCAGGGAGGAATTCAGGTGCTCAAGAGAAAGATATATTAAACAGCTTTCATCTGGT 3399  
QY 1055 SerLeuLeuGlyTyArg-----LysTyGlnProAsnIleAsp-----Val 1068  
Db 3400 CGTGTGTGGAAATCCAAACAATCTGCAATGACTATGTCATATGCTAGACAGCAGCAT 3459  
QY 1069 GlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyThr 1088  
Db 3460 AAGAGGCCCAAAATTTACTCAAAAGATGAGAAA---CTGCAAGGCCTTACT 3516  
QY 1089 LeuAlaLeuIleThrTyAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeu 1108  
Db 3517 ACAGCCCTCACAGCTATGCTTTGGCT-----GCTGCAGACCAACTC 3558  
QY 1109 AsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpValSerSerGlu 1128  
Db 3559 AATGATGACAGGTACTCATGCGCAGCATCAACAGGAAGGATCATTTGG----- 3606  
QY 1129 SerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyAla 1148  
Db 3607 -----GAAGAATAACAATGCTCACACCCACCAACATTGAAGGCCTTCTCTATGCC 3654  
QY 1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168  
Db 3655 TTGTGTCCCTGTGAAATGAAGAAATTTGATCAAACTGGTCCCATAGTCAGATGGCTG 3714  
QY 1169 SerArgGlnArgAsnSerLeuGlyPheAlaSerThrGlnAspThrThrValAlaLeu 1188  
Db 3715 ACAGATCAGAAATTTTATGGGAAACATATGGACAAACCCCAAGCAAGTATGGCAATT 3774  
QY 1189 LysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArg---ThrAsnIleGlnVal 1207  
Db 3775 CAAGCTCTTGTGAATATGATTCAGATCGCTACCATTAAGGACTTTAAACTTAGATATT 3834  
QY 1208 ThrValThrGlyProSerSerProSerProLeu----- 1218  
Db 3835 ACTATTGAATGCCAGATCGAGATGATCTATTAGGTACAGAAATTAATTTGAAAATGCT 3894  
QY 1219 -----AlaValValGlnPro-----MetAlaValAsnIleSerAlaAsnGly 1232  
Db 3895 CTCCTGGCTCGACAGTAGAGACCAAACTCAACCAAGACATCACTACTGTGACGATCAGGT 3954





207 ---GlnValGlnValAspGlnThrTyrTyrGlnSerPheGlnValSerGluTyrVal 225  
QY  
Db  
604 GCCAAATATGAACATCCCGAGAAATATACCTGATATTTGATGTTCAGAAATATG 663  
QY  
Db  
226 LeuProLysPheGluValThrLeuGlnThrPro-----LeuTyrCysSerMetAsn 242  
QY  
Db  
664 TTGCCAAGCTTTGAAGTCCGCTGCAACACCATGAGAGTCTTTGATGGAGAGTGAAGGT 723  
QY  
Db  
243 SerLysHisLeuAsnGlyThrLeuAlaLysTyrThrTyrGlyLysProValLysGly 262  
QY  
Db  
724 ---GAAATTTCCACGTGCTATACCTGCAAGGTACTTTGATGGAGAGTGAAGGT 780  
QY  
Db  
263 AspValThrLeuThrPheLeuProLeuSerPheTyrPheGlyLysLysAsnIle----- 280  
QY  
Db  
781 ---GTGGCCCTTTGCTCTTTGAGTGAAATAGATGATGCTATAAAGAGTATTCAGAC 837  
QY  
Db  
281 ---ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGlu 298  
QY  
Db  
838 TCACTCAGAGATTCGGATATTGATGGAGATGGGAAGCAACACTAAAGAGATACA 997  
QY  
Db  
299 MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro 318  
QY  
Db  
898 TTCCGTTCTCGATTTCCAAATCTCAATGAGCTTTGTTGGGCATACTCTGATGCATCT--- 954  
QY  
Db  
319 GlyProValGluLeuLeuThrThrValThrGluSerValThrGlyLysSerArgAsnVal 338  
QY  
Db  
955 ---GTAACAGATCATGACAGAAATCAGCGAGTATATGATGACTGAG 999  
QY  
Db  
339 SerThrAsnValPhePheLysGlnHisAspTyrIleLeuGluPheAspTyrThrThr 358  
QY  
Db  
1000 CAAAGCGCATTCATATGTTGGCATCTCCCTATCAGATCCACTTCACAAAACCCCAAA 1059  
QY  
Db  
359 ValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn 378  
QY  
Db  
1060 TATTTCAAGCCAGGAATGCCATATGAACCTGACGCTGTATGTTACCAACCTGATGCTCA 1119  
QY  
Db  
379 GlnLeuThrLeuGluGluArgAsnAsnValIleThrValThrGlnArgAsnTyr 398  
QY  
Db  
1120 CCAAGCT-----GCCATGTGCCAGTGTGTATCAGAGGCCCTTT 1155  
QY  
Db  
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Db 3955 GATGAAAAGCAAAATGACATTTTGCATCTTATTAACGCCAGTTG----- 4002  
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QY 1322 LysValGluTyrAspHisGlyLysLeuAsn-----LeuTyrLeuAspSer 1336  
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RESULT 14  
US-08-447-411-75  
; Sequence 75, Application US/08447411  
; Patent No. 5773243  
; GENERAL INFORMATION:  
; APPLICANT: FRITZINGER, DAVID C.  
; APPLICANT: BREDEHORST, REINHARD  
; APPLICANT: VOGEL, CARL-WILHELM  
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,411  
; FILING DATE: 07-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5773243man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-101-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 75:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..4001  
US-08-447-411-75

Alignment Scores:  
Pred. No.: 3,66-72 Length: 4138  
Score: 768.50 Matches: 306  
Percent Similarity: 41.88% Conservative: 212  
Best Local Similarity: 24.74% Mismatches: 465

Query Match:	10.46%	Indels:	255	
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369 ThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsn	388			
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389 ValValIleThrValThrArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGly	408			
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165 CATGTGCCAGTGGTATCAGAGGCCATTCATCTGAG	203			
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204 ACCACTTTGATGGGACTGTAAAGCTCTCTCGAACACACACAAAATGCTCAA	260			
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429 LysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu	448			
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Qy				
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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-662-227-33

Alignment Scores:  
Pred. No.: 3,6e-72 Length: 4138  
Score: 768.50 Matches: 306  
Percent Similarity: 41.88% Conservative: 212  
Best Local Similarity: 24.74% Mismatches: 465  
Query Match: 10.46% Indels: 255  
DB: 2 Gaps: 46

US-10-020-095-4 (1-1428) x US-08-662-227-33 (1-4138)

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DB 66 TATCAGATCTACTTACAAAACCCCAAAATATTTCAGGCAGGATGCCATATGAAC 125  
QY 369 ThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsn 388  
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QY 389 ValValleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSergly 408  
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QY 429 LysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu 448  
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QY 449 GlySerLysSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIle 468  
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QY 469 GlnLeuLysThrArgAspGluAsnIleLysValGlySer 486  
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QY 535 TyrIleGluAspGlyGluIleIleSerAspValLeuLysIleProValGln----- 552  
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QY 553 -----LeuValPheLys-----AsnLysIleLysLeuTyr 562  
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DB 726 -----CCAGGAGCTGCAATGAAATCAAAATTTGGAA-----GGGGAT 761  
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QY 960 GlyTyrGlnArgGlnLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsn 979
Db 2154 GGTATGCCACAGTGTGTGACAAAGAACAGACCATCTCTATGACACATTTACAAAC 2213
QY 980 TyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPhe---LeuGlu 998
Db 2214 -----AGTGCATCTAGTCTTGGCTACAGCATATGTTGTAAAAATCTTTGCCITGGCT 2267
QY 999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu--- 1017
Db 2268 GCCAAAATTTGTAAGACATTAACCATGAATCGTTTGTGGAGTATGAGGTGGCTGATT 2327
QY 1018 LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 1037
Db 2328 CTGAACAGGCAACAGACAGATGAGTGTTCAGAGAAAGCCCTGTACTTTTGGAAACA 2387
QY 1038 LeuGlnGlyGlyAsnLysSerProVal-----ThrLeuThrAlaTyrIleValThr 1054
Db 2388 ATCAGGGAGGCATTCAAGGTGCTGAACACAGAGGATCTTTACAGCTTTTCACTCTGTT 2447
QY 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074
Db 2448 GCCTGTGTGAATCCAGATCAATC-----TGCAATGCATATATCATATTT 2492
QY 1075 LeuGluSerGluPheSerArgGly-----LeuThrTrpArgAlaGluGlnGlyGlyMetG1 1084
Db 2493 CTAGACAGCAGCATCAGTAGGCCACAGATTATTTACTCAAAAAGTATGAGAACTGCAA 2552
QY 1085 AspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAla 1104
Db 2553 AGGCCTTACACTACAGCCCTCACAGCCTATGCTTGGCT-----GCT 2594
QY 1105 LysGluAlaLeuAsn-Met-----LeuThrTrpArgAlaGluGlnGlyGlyMetG1 1122
Db 2595 GCAGAACGATCATATGATGACAGGTACTCATGGCAGCATCACAGGAAGGA----- 2646
QY 1122 nPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspI1 1142
Db 2647 -----ATCGTTGGGAAGAACCTTAACGCCACACCCATAAC-AT 2683
QY 1142 eGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyI1 1162
Db 2684 TGAAGGCACCTTCCTATGCTTGTGTGGCCCTGCTGAAAATGAAGAAATTTTGGAGCCGG 2743
QY 1162 eProfileMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrG1 1182
Db 2744 TCCTGTAGTCCAAATGGCTGATGATCAGCAATATTATGGGGGAACATATGGACAAACCCA 2803
QY 1182 nAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaLeuMetAsnThrGluAr 1202
Db 2804 AGCAACAGATTATGATGTTTCAAGCTCTTGCTGAATATGAGATTTCAGATGCTACCCATAA 2863
QY 1202 g---ThrAsnIleGlnValThrValThrGlyProSerSerProSerPro----- 1217
Db 2864 GGACTTAAACTTAGATATTACTATTGTAACTCCAGATCGAGAAGTACTCTATAGGTACAG 2923

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QY 1218 -----LeuAlaValValGlnProMetAlaValAsn----- 1227
Db 2924 AATTAAATTATCAAAATCCTCTCTGGCTCAGACAGTAGAGCAACCAACTCACGAAGACTT 2983
QY 1228 ---IleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnVa 1246
Db 2984 CACTGTGTCAGCATCAGGTGATGAAAAGCAACAATGACCATTTTGACGGTCTATAATGC 3043
QY 1246 lLysAlaSerGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLe 1266
Db 3044 ACAATTG-----AGGGAGGATGCAAAATGTTTGCACAAA-----TTCCATCT 3085
QY 1266 uAspValAlaVal-----LysGluAsnLysAspAspLeuAsnHi 1279
Db 3086 TGAITTTTCTTTGAAAACGTCAGTTGAATTAARAAGACCAAGGAGCCAGGGAGC 3145
QY 1279 sValAspLeuAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMe 1299
Db 3146 CTTCAAGCTCAAAATCTGCATAGGTATCTGGGAGAAAGTTGATTCTACAATGACAAATA 3205
QY 1299 tGluValAsnLeuLeuSerGlyPheMetValProSerGluAlaIleSer---LeuSerG1 1318
Db 3206 TGATGTTTCTATGCTGACTGTTTGTCCCTGATCTAGACACCTTACGAGGCTTTCTAA 3255
QY 1318 uThrValLysLys-----ValGluTyrAspHis-----GlyLY 1329
Db 3256 AGGAGTCGACAGATATATCTCCATGTTTGAATTAACAATAATATGGCTCAGAAAGGAAC 3325
QY 1329 sLeuAsnLeuTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAl 1348
Db 3326 TGTATATCTTTACTTAGACAAGGTCTCCACTCTGAAAGATGAATGCCCTGCACCTTAAGAT 3385
QY 1348 aValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTY 1368
Db 3386 TCTCAAGCATTTTGAAGTTGGCTTCATTCAGCCAGGATCAGTCAAGGTGTACAGCTACTA 3445
QY 1368 rGluProArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAs 1388
Db 3446 CAATCTAGATGAAAAATGTACCAAGATCTACCATCCAGATGAAGCAACAGGCCTTCTCAA 3505
QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAlaSer 1404
Db 3506 TAAGATATGTGTGTGTAACGTTTGGCGATGTGCAGAGAAACCTGTTCC 3554

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Search completed: August 18, 2004, 05:37:38  
Job time : 718 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2004, 19:31:34 ; Search time 57 seconds  
(without alignments)  
7858.583 Million cell updates/sec

Title: US-10-020-095-4  
Perfect score: 7348  
Sequence: 1 MQGPPLTAAHLLCVCTAAL.....HSSVIFPCKLLYFMELWL 1428

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3360	45.7	665	15	US-10-108-260A-3396
2	2962.5	40.3	596	12	Sequence 3396, Ap
3	1854.5	25.2	1508	15	US-10-112-944-404
4	1850	25.2	1519	15	US-10-369-493-5314
5	1628.5	22.2	336	15	Sequence 5314, Ap
6	1592	21.7	352	12	Sequence 5313, Ap
7	1542.5	21.0	1979	15	Sequence 2445, Ap
8	1539.5	21.0	1885	15	Sequence 1951, Ap
9	1529.5	20.8	1927	15	Sequence 30, Appl
10	1491	20.3	1476	12	US-10-085-198-30
11	1491	20.3	1476	12	US-10-085-198-28
12	1441	19.6	1474	12	US-09-972-211-69
13	1441	19.6	1474	12	US-10-096-625-69
14	1441	19.6	1474	12	Sequence 69, Appl
15	1441	19.6	1474	13	Sequence 65, Appl
					Sequence 65, Appl
					Sequence 15, Appl
					Sequence 2, Appl1

16	1441	19.6	1474	14	US-10-292-081A-15	Sequence 15, Appl
17	1440	19.6	1474	9	US-09-873-403-5	Sequence 5, Appl
18	1440	19.6	1474	12	US-09-972-211-66	Sequence 66, Appl
19	1440	19.6	1474	12	US-10-170-385-405	Sequence 405, App
20	1440	19.6	1474	12	US-10-096-625-66	Sequence 66, Appl
21	1440	19.6	1474	12	US-10-608-397-10	Sequence 10, Appl
22	1440	19.6	1474	12	US-10-608-397-12	Sequence 12, Appl
23	1440	19.6	1474	12	US-10-608-397-13	Sequence 13, Appl
24	1440	19.6	1474	12	US-09-750-972-5	Sequence 5, Appl
25	1440	19.6	1474	14	US-10-292-081A-10	Sequence 10, Appl
26	1440	19.6	1474	14	US-10-292-081A-12	Sequence 12, Appl
27	1440	19.6	1474	14	US-10-292-081A-13	Sequence 13, Appl
28	1440	19.6	1474	15	US-10-331-496A-38	Sequence 38, Appl
29	1437.5	19.6	1508	10	US-09-756-247-4	Sequence 4, Appl
30	1436	19.5	1458	12	US-10-096-625-200	Sequence 200, App
31	1433	19.5	1450	10	US-09-756-247-23	Sequence 23, Appl
32	1433	19.5	1491	10	US-09-756-247-25	Sequence 25, Appl
33	1428	19.4	1500	12	US-10-608-397-9	Sequence 9, Appl
34	1428	19.4	1500	14	US-10-292-081A-9	Sequence 9, Appl
35	1421.5	19.3	1492	11	US-09-981-151A-10	Sequence 10, Appl
36	1421.5	19.3	1492	12	US-09-972-211-2	Sequence 2, Appl
37	1421.5	19.3	1492	12	US-10-096-625-2	Sequence 2, Appl
38	1419	19.3	1451	10	US-09-756-247-24	Sequence 24, Appl
39	1417.5	19.3	1450	12	US-10-037-417-113	Sequence 113, App
40	1413.5	19.2	1450	12	US-09-972-211-67	Sequence 67, Appl
41	1413.5	19.2	1450	12	US-10-096-625-67	Sequence 67, Appl
42	1412.5	19.2	1472	12	US-09-972-211-68	Sequence 68, Appl
43	1412.5	19.2	1472	12	US-10-096-625-68	Sequence 68, Appl
44	1406.5	19.1	1476	12	US-10-037-417-114	Sequence 114, App
45	1395	19.0	1473	12	US-10-037-417-112	Sequence 112, App

ALIGNMENTS

RESULT 1  
US-10-108-260A-3396  
; Sequence 3396, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: HL-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3396  
; LENGTH: 665  
; TYPE: PNT  
; ORGANISM: Homo sapiens  
US-10-108-260A-3396

Query Match 45.7%; Score 3360; DB 15; Length 665;  
Best Local Similarity 100.0%; Pred. No. 2.4e-267;  
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQGPPLTAAHLLCVCTAALAVAPGPRFLVTAPGIIIRPGNVITIGVLELHCPQSVTVKA	60
Db	1	MQGPPLTAAHLLCVCTAALAVAPGPRFLVTAPGIIIRPGNVITIGVLELHCPQSVTVKA	60
Qy	61	ELLKTASNLTVSVLEAEGVFEKSGFKTLTLPSPLSADEIYELRVGTGRTODELIFNST	120
Db	61	ELLKTASNLTVSVLEAEGVFEKSGFKTLTLPSPLSADEIYELRVGTGRTODELIFNST	120
Qy	121	RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDPKPKYKTSNLIKDKPSNLIQOWL	180
Db	121	RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDPKPKYKTSNLIKDKPSNLIQOWL	180
Qy	181	SCQSDLGWISKTFOLSSHPILGDWSIQVNDQYQSFQVSEYVLPKFEVTLQPLYCS	240
Db	181	SCQSDLGWISKTFOLSSHPILGDWSIQVNDQYQSFQVSEYVLPKFEVTLQPLYCS	240

QY 241 MNSKHLNGTITAKTYGKPVKGDVTLTFLPLSPGWKKNIITKTFKINGSANTSFNDEEMK 300  
 Db 241 MNSKHLNGTITAKTYGKPVKGDVTLTFLPLSPGWKKNIITKTFKINGSANTSFNDEEMK 300  
 QY 301 NVMDSNGLSEYLDLSPGVEILTTVTESVTGISRNVSTNVFFKQHDYIIIEFFDYTTVL 360  
 Db 301 NVMDSNGLSEYLDLSPGVEILTTVTESVTGISRNVSTNVFFKQHDYIIIEFFDYTTVL 360  
 QY 361 KPSLNFTATVKVTRADGNQTLTLEERNVVTITQRYTEYKSGNSGNQKMEAVOKINY 420  
 Db 361 KPSLNFTATVKVTRADGNQTLTLEERNVVTITQRYTEYKSGNSGNQKMEAVOKINY 420  
 QY 421 TVPSQGTFFKIEFFILEDSSSELQKAYFLGSKSMVHSLFKSPSKTYIQLKTRDENIKVG 480  
 Db 421 TVPSQGTFFKIEFFILEDSSSELQKAYFLGSKSMVHSLFKSPSKTYIQLKTRDENIKVG 480  
 QY 481 SPPELVSGNKLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYIEDDG 540  
 Db 481 SPPELVSGNKLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYIEDDG 540  
 QY 541 EIIISDLVKIPVQLVFNKIKLYMSKVAEPSEKVSRLRISVTQPDSDIVGIVAVDKSVNLNM 600  
 Db 541 EIIISDLVKIPVQLVFNKIKLYMSKVAEPSEKVSRLRISVTQPDSDIVGIVAVDKSVNLNM 600  
 QY 601 ASNDITMENVHLELYNTGYIIGMFNMFNPAVFQECGLWVLTDLNLTQDYIDGVYDN 657  
 Db 601 ASNDITMENVHLELYNTGYIIGMFNMFNPAVFQECGLWVLTDLNLTQDYIDGVYDN 657

## RESULT 2

US-10-112-944-404  
 ; Sequence 404, Application US/10112944  
 ; Publication No. US20040048249A1

## GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Yang, Yonghong  
 ; APPLICANT: Wang, Gezhi  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Wehrman, Tom  
 ; APPLICANT: Ghosh, Malabika  
 ; APPLICANT: Wang, Dunrui  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Wang, Zhiwei  
 ; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and  
 ; TITLE OF INVENTION: Secreted Polypeptides  
 ; FILE REFERENCE: 805A  
 ; CURRENT APPLICATION NUMBER: US/10/112,944  
 ; CURRENT FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/491,404  
 ; PRIOR FILING DATE: 2000-01-25  
 ; PRIOR APPLICATION NUMBER: US 09/496,914  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: US 09/515,126  
 ; PRIOR FILING DATE: 2000-02-28  
 ; PRIOR APPLICATION NUMBER: US 09/519,705  
 ; PRIOR FILING DATE: 2000-03-07  
 ; PRIOR APPLICATION NUMBER: US 09/540,217  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: US 09/552,929  
 ; PRIOR FILING DATE: 2000-04-18  
 ; PRIOR APPLICATION NUMBER: US 09/577,408  
 ; PRIOR FILING DATE: 2000-05-18  
 ; NUMBER OF SEQ ID NOS: 924  
 ; SOFTWARE: pt\_FL\_genes Version 5.0  
 ; SEQ ID NO 404\_

; LENGTH: 596  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-112-944-404

## Query Match

40.3%; Score 2962.5; DB 12; Length 596;  
 Best Local Similarity 96.2%; Pred. No. 1.2e-234;

Matches 587; Conservative 0; Mismatches 2; Indels 21; Gaps 1;

QY 1 MQGPPLTAAHLLCVCTAALAVAPGPRFLVTAPGIIIRPGGNVTIGVELLEHCHSPQVTVKA 60  
 Db 1 MQGPPLTAAHLLCVCTAALAVAPGPRFLVTAPGIIIRPGGNVTIGVELLEHCHSPQVTVKA 60  
 QY 61 ELLKTASNLTVSVLEARGVEKGSFKTLTLPSPLSNADAEIYELRVTRGTRQDEILFSNST 120  
 Db 61 ELLKTASNLTVSVLEARGVEKGSFKTLTLPSPLSNADAEIYELRVTRGTRQDEILFSNST 120  
 QY 121 RLSFETKRISVFIQTDKALYKQEVKFRIVTLFSDDFPKYKTSNLILIKDPKSNLIQQWL 180  
 Db 121 RLSFETKRISVFIQTDKALYKQEVKFRIVTLFSDDFPKYKTSNLILIKDPKSNLIQQWL 180  
 QY 181 SQQSDLGVISKTFQLSHPILGDSIQVNDQTYQSFQVSEYVLPKFEVTLQTPUYCS 240  
 Db 181 SQQSDLGVISKTFQLSHPILGDSIQVNDQTYQSFQVSEYVLPKFEVTLQTPUYCS 240  
 QY 241 MNSKHLNGTITAKTYGKPVKGDVTLTFLPLSPGWKKNIITKTFKINGSANTSFNDEEMK 300  
 Db 241 MNSKHLNGTITAKTYGKPVKGDVTLTFLPLSPGWKKNIITKTFKINGSANTSFNDEEMK 300  
 QY 301 NVMDSNGLSEYLDLSPGVEILTTVTESVTGISRNVSTNVFFKQHDYIIIEFFDYTTVL 360  
 Db 301 NVMDSNGLSEYLDLSPGVEILTTVTESVTGISRNVSTNVFFKQHDYIIIEFFDYTTVL 360  
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 Db 361 KPSLNFTATVKVTRADGNQTLTLEERNVVTITQRYTEYKSGNSGNQKMEAVOKINY 420  
 QY 421 TVPSQGTFFKIEFFILEDSSSELQKAYFLGSKSMVHSLFKSPSKTYIQLKTRDENIKVG 480  
 Db 421 TVPSQGTFFKIEFFILEDSSSELQKAYFLGSKSMVHSLFKSPSKTYIQLKTRDENIK-- 478  
 QY 481 SPPELVSGNKLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYIEDDG 540  
 Db 479 -----VVSRLGQLVAVGKQNSTMFSLTPENSWTPKACVIVYIEDDG 519  
 QY 541 EIIISDLVKIPVQLVFNKIKLYMSKVAEPSEKVSRLRISVTQPDSDIVGIVAVDKSVNLNM 600  
 Db 520 EIIISDLVKIPVQLVFNKIKLYMSKVAEPSEKVSRLRISVTQPDSDIVGIVAVDKSVNLNM 579  
 QY 601 ASNDITMENV 610  
 Db 580 ASNDITMENV 589

## RESULT 3

US-10-369-493-5314  
 ; Sequence 5314, Application US/10369493

; Publication No. US20030233675A1

## GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 5314  
 ; LENGTH: 1508  
 ; TYPE: PRT  
 ; ORGANISM: Caenorhabditis elegans

US-10-369-493-5314

Query Match	25.2%	Score 1854.5;	DB 15;	Length 1508;
Best Local Similarity	31.8%	Pred. No. 1.3e-142;		
Matches 476;	Conservative 292;	Mismatches 562;	Indels 169;	

Qy	15	VCTAALAVAPGRELVTAPGIIRPGGNVTIGVBLEHCPCSVQTVKAEILLTKTASNLTVSVL	74
Db	28	VSTTAAAPVKPA-TYMLVAPAVRDPQPSVCMNLLKQATDEMDMLVREIVERTNETAAR	86
Qy	75	EAGGVFEKSGFKTULTSLPNSAD--EIVELRVGTQD-EILFSNSTRLSFPTKISV	131
Db	87	VISNL-REGIAQTVSLSEMPAQSLTPRSYKLYIRGETLNAELIFENENELKYQKALS	145
Qy	132	FIQTDKALYKPKQEKPRIVTLFSDFPYKTSMLILKDPKSNLIIQWLSSQSDLGWISK	191
Db	146	FIQDRAIYRPAISLVRYRAIVKVSDLKPYVGNATIKIFDPSGRNLISQITIGVTLDRGYSG	205
Qy	192	TFQSSHPILGDWSIQVQ---VNDQTVYQSFQVSEYVLPKFEVTLTQPLCYSMNSKHLN	247
Db	206	ELQLABETLLGDWIEVETSGVQDKS---SFTVDVTYVLPKFEVNIKTSPFIIND-DLS	261
Qy	248	GTITAKTYKPKVGDVTLTF-LPLSTW-----GKKKN-----TKTKFIN--GS	288
Db	262	VFDQAKTYGKGVAGKAKVSLLEPWHRHAMVPTIIDENGVKKEELMVERTVKLNQGE	321
Qy	290	ANPFDNBEKMNVDSSNGLSEYLDLSSPGPVEILTTVTSVTCIGSRNVSTNVFFKQHDY	349
Db	322	AAVFSNDELKR-----HKLHEWGGGSIIRIVASVTEIDITEIERNATHOISTPREV	373
Qy	350	IIIEFDVTVLKPSLNFATVKKVTRADGN--QLTEERRNNVLTITQRYNTYVWSGNS	407
Db	374	KLDVEKQGDTFKPGLTIVNVVALKQMDPTPKATLPKR---QVSTFYNYP--YNHDT	427
Qy	408	GNQKWEAVOKINVTVPQSGTFKIEPFFILEDSSELQKAYFLGSKSSMAVHSLFK-----	461
Db	428	SLQBEKETKIVEVDAGTGSVLTQPLPINCTSARIEAH-YDIGGKDNFTATPISLSLYEA	486
Qy	462	--SPSKYVIQLKTRDEN-IKVGSFFELVNSKNKLKLSYVWVSRGOLV-----AVGKN	513
Db	487	AVSPKTSFLQLLANEGADVKGKSLSPSLKATQPLSTITYQVMSRNIWVSQOQTVNSEH	546
Qy	514	STMSPLTPENSWPKACIVIV-YTEDGGEIISDVLPKIPVOLVFKNKIKLYMSKVKAPSE	572
Db	547	ATI--SFPATANMAFKSLIVVAIIESQEVLDALDFKVEGIFQNVALSIDKQAVBPQ	605
Qy	573	KVSLRISVTPQDSIVGVAVDKSVNLMNASNDIMENVWHELELYNTGYVLGMF-----	626
Db	606	NVRPKVT-SDKNSFVGLVWDQSVLLKTGNNDITREKVEQOLENYDNNVGGSGGPRPW	664
Qy	627	-----MNSFAVFCBGLWLVTDLMLTKD-----YIDGVYDNA	658
Db	665	EADREKXRSIWRPWWGCGSDAQISFNAGLVLTDLALREPOREFWMSVMMMDCAPMA	724
Qy	659	EYAEFRMEENEGHIVDTHDFSLGSS---PHVKRHPPTWIWLDTNMGYRIYQFEVTPVD	715
Db	725	EAA--FAAPMG-----GSSPPPTVKRFPPTWIWSDLN-STSGEVEMEIBAPD	771
Qy	716	SITSWATGFVISDLGLGTLTTVEVLOAFOPFIPLNPLYSVIRGEEFALEITFNULK	775
Db	772	TITSWASTAINEENGLGVAPTISKLRVFPFIQLNLPYAVRGEKFKALLVLFVNYME	831
Qy	776	DATEVKVII--EKSDFDILMTSSEI---NATGHQQTLLVPSEBGAT---VLPFIRPTRL	827
Db	832	KEQDVTVTLKYDKDSGYDLLKDGTVVRDEVGQONRIVSVAGGGTSKAYFPIVPS	891
Qy	828	GEIPITVATLSPASDAVTQMLVKARGIEKYSQSILLDLDNRLOSTLTKTSLFSFPPN	887
Db	892	GEIPVHISATASQCGDAVENMLRVDPOGVKVDNRNIPFVIDUNNNSDFS-KNLELIWPD	950
Qy	888	TVTGSERVQITAGDVLGPSINGLASIRMPYGCGEQNMINFAPNIYILDYLTKKKQOLD	947
Db	951	VVDGSGQARLDVIGDMMPVLNNAHKLVQVPGCGEQLMNLVFNILVWVKYLRATINNES	1010

## RESULT 4

```

US-10-369-493-5313
; Sequence 5313, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5313
; LENGTH: 1519
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5313

```

Query Match	25.2%	Score 1850;	DB 15;	Length 1519;
Best Local Similarity	31.6%	Pred. NO. 3e-142;		
Matches 477;	Conservative 290;	Mismatches 563;	Indels 180;	Gaps 44;

Qy	15	VCTAALAVAGPRLVTAQGIIPGGNVTTGVLELHECPQSVTVKABLLKTASNLTVSVL	74
Db	28	VSTIAAPVKFA-TYMLVAPAVAPDPQFSCVMNLLKQATDEDMIVRTEVTRNETNTAAR	86
Qy	75	EAGGVFEKSGFKTLTPSLPLNSAD--EYELRVGTGTQD-EILFSNSTLSFETKRIISV	131
Db	87	VISNL-KPGIAQTVSISEMPAQSLTPRQSYKLYIRGETLMAELIFENENELKYDQKALSV	145
Qy	132	FIQTDKALYKPKQEVKFRIVLTLSDFSPYKTSNLIKDKPKSNLIOQLSQSDLGVIISK	191
Db	146	FIOIDRAIPASLIRVRA-VKASDLKPYGVGNATIKTFDPSRNLIISOTIGVTLDRGVYSG	205



[illegible]

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US-10-085-198-30
; Sequence 30, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20

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664 PMENEGHIVDIDHDSIGSGFH-----VRKHFFETWIDTNGYRIYQ-EFEVTVPD 715  
813 AFQPHGTSLV-----AVAPSRHPRTEKRRTPPETWICHLNISDPGEGTSLVKVPD 867  
716 SITSWATGVISEDLGLGTTTTVELQAPOPFFIFLNLPSYVIRGEFEFALETTIPNLYK 775  
868 SITSWGEAVALSTSQLGI-APESLLKTKPFVDFVDFMLPALLIRGEQVKIPLSVNYNG 926  
776 DATEV--KVIIEKSKDPDILMTSEINATG-----QOTLLVPSDEGATVLPFRPHL 827  
927 TCAEVYMKLSVPKGIQF-----VGHGKRHVTKKWCVPAGEAFPWWVLSFSL 975  
828 GEIPITVIALS-----PTASDAVOTMILVKAEGIEKSYQ 862  
976 GLNNITAKALAYGDTNCCDRGSKHPEENHADRVPDGVDRVRSVMVEAGVPRAYTY 1035  
863 SIL-----LDLT-----DNRL----- 873  
1036 SAFPCPSRVHISTPNKYEQYVQRPULRTRFDVAVRAHNDARVALSSGPQDTAGMIEIV 1095  
874 -----QSTLKTLSF----- 882  
1096 LGHQNTRSWISTKMGEPVASAHTAKILSDDEFRTWISWRGGLIQVGHGPEPSPNESVI 1155  
883 -----SFPNTVTGSRVQIT 898  
1156 VANTLPRPPEVQIFGFTGWSMGEFRINRMEVDESYSFAFTLGVPHGAIPGSRATAS 1215  
899 AIGDVLGPIASLIRMYGCGEQMINFAPNIVILYTKKQITDNLKEKALSFR 958  
1216 IISDMGPTLHNLRLPFGCGEQNMIFAPNIVFLKYLQTKQSLPEVERETTYDILV 1275  
959 QGYORELLYOREDSFGAFGNYPGSGTSLSAFVLRFCLEADPYDIDQNLVHRTVTLK 1018  
1276 QGYORQTYKRDGYSAFGERDASGSMWLTAVLKSFAQARSFIFVDRFLAAKSII 1335  
1019 GHKSNGEFDPGRVHSELQGNKSPVTLTAYITVSL--GYRKYQPNIDVOESIHFL 1076  
1336 QQQQADGSLAVGLVNLKIQGGIHGVPLTAYVVALLETGTASSEERGSTDKARHFL 1395  
1077 SEPSRGISDNVTLALITYALSSVSPKAEALNMLTWRAEQEGMQFVWSSKLSDSQ 1136  
1396 SAAPLAW-DPYSICALITYALTLLRSPAPEALRKLRLSLAIRMGGVTHW-----SLSNSWD 1449  
1137 PR-----SLDIEVAAYALLSHFLQFQTSSEGIPIRMLWRQNRSLGFPAS 1180  
1450 VDKTFLSFDVRSQSVSAEVMETAYALLTYLLGDAALPVKWLSQLQNALGGFSS 1509  
1181 TQDTTVALKALSEPAAL-----MNTERTMIOVTVG--PSSPS 1216  
1510 TQDTCVALQALAEYAILSYAGGINLTVSLASTNLDYOETPELHRTNQVLQTAAPSLPT 1569  
1217 PLAVVQPMVANNISANGFGAICOLNVVNYVK--ASGSSRRRSIQOE----- 1262  
1570 GLFV-----SAKGGCCLMIDVTYVDPVAKPAFOLLVSLQEPAGRPMPAS 1621  
1263 -----AFDLVAVKENKDDLNDLVNCTSPSGRSGMALMEVNLISGFWVPS 1311  
1622 AAGSRGDWPPADDDPAADQHHOEYK-VMLEVCTRHLHAGSSNMAVLEVPILLSGFRAI 1680  
1312 EAILSSET-----VKKVEYDHGKLNLYDSV-NETQFCVNIPAVNPKVSNQDASVS 1363  
1681 E--SLEQLLLDKHGMKRYEVAGRVULFYDEIPSRCLTCVRFEALRECVGRTSALPVS 1738  
1364 IDVYEPQRQAVRSYNEV-----KLSSCDLSDVQ-----GCRPCSDGASGSHHS 1410  
1739 VDYDEPAFAETRFYNYSTHSPARELCAGPACNEVERAPARGPFGWPGSGPAVAPEEG 1798  
1411 SVI 1413  
1799 AAI 1801

RESULT 8  
US-10-085-198-28  
; Sequence 28, Application US/10085198  
; Publication No. US2004000907A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook et al.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-279  
; CURRENT APPLICATION NUMBER: US/10/085,198  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/271,646  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/276,401  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/311,981  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/312,858  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/271,840  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/277,324  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/286,096  
; PRIOR FILING DATE: 2001-04-21  
; PRIOR APPLICATION NUMBER: 60/299,695  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/315,614  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/272,405  
; PRIOR FILING DATE: 2001-02-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 653  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 1885  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-085-198-28  
Query Match 21.0%; Score 1539.5; DB 15; Length 1885;  
Best Local Similarity 27.3%; Pred. No. 1.7e-116;  
Matches 493; Conservative 257; Mismatches 556; Indels 497; Gaps 57;  
QY 5 PLLTRAHLVCV-----TAAAVAPGPRFLVTAAGIIRPGGNVTIGVELLHCHPSQVTVKA 60  
DB 8 PLLPILLLLLSARGDGVRAAQPAFG--YLIAAPSVFRAGVEEIVSVTIF-NSPREVTVQA 64  
QY 61 ELLKTASNLTVSLEAEG-VPEKGSFKTLTLPSLPLNSADEIYELRVTVGR---TQDEILF 116  
DB 65 QLVAGE-----PVVQSQAILLDKGTIK-LKYPTGLRGQA-----LLKVMGRGWAEGPLF 115  
QY 117 SNSTRLSFETKRIISVFTQTKALYKPKQEVKFRIVTLFSDFKPKYKTSINILIKDKPSNLI 176  
DB 116 HNOTSVTVDRGASVFIQTDXPVYRQHRVLISFTVSPNLRPNVNEKLEAVILDPGRSRM 175  
QY 177 COWLS-QQSDLGVTSKTLPOLSSHPILDGWSIQOVNDQTYQSPQSVSEYVLPKFEVTLQT 235  
DB 176 IEWRHLKFCGCIITMSFPLSDQPVLGWFIFVEMQGHAYNKSFEVQKYVLPKPELLIDP 235  
QY 236 PLYCSMNSKHLNGITAKYTKPKVKGD--VTLLFPLPSFWGKK--KNITKTFKINGSAN 291  
DB 236 PRYIQQLDACETGTVRARTFTGPKFVAGALMINMTVNGVYTSHEVGRPVLRTTKILGRD 295  
QY 292 ISFDEENKMNVDSSNGLSEYLDLSSP---GPVEILLTVTSTVGTISRNVTNVFFKQH 347  
DB 296 FDIQVDRM-----IPADVPEHFRGRVSIWMT-SVDSGQQ----- 330  
QY 348 DYIIEFFDYTTY-----LKPSLNFTATVKVTRADGNQLTLEBRNNVVI 391  
DB 331 ---VAFDDSTFVQRQLVDIRYSKOTRKQFKPLGAYVGVKVELSYDPGSP-----AEGTV 381  
QY 392 TVTQRNYTEYSGNSGNQKWEAVQKIN-VT---VPQSGTFKIEFPILDESSE---LQLK 444





103 E-----LRVTGR---TODEILFSNSTRLSFETKRSISVFIQTDKAL 139  
121 PVLRYFQKQGVPTGLRGQALLKVGWGWQAEBCPLFHNQTSVTVDRGASVFIQTDKPV 180  
140 YKPQKQEVKFRIVTLFSPDKPKYSNLNLIKDPKSNLIQWLS--QQSDGLGVISKTFOSSH 198  
181 YRQHRVLIISIFTVSPNLRVFNKLEAYILDPGRSMIEWHLKPFCCGTTNNSFPLSDQ 240  
199 PILGDSIQVQVNDQTYQGFQVSEYVLPKFEVTLQTPLYCSMNSXHLNGTIITAKTYGK 358  
241 PVLGEWIFVEMQCHANKSFEVQKVLPAFELLIDPPRIQDLDACEITGVREARYTFCG 300  
259 PVKGD--VTLTFLPLSPWKK--KNITKTPKINGSANFSENDEKMNVDSSNGLSEYLD 314  
301 PVAGALMINMTVNGVGYSHVEGRPVLRITTKILGSRDFDICVRDM-----IP 347  
315 LSSP---GPVELLTVTESVTGFSRNVSTNVFFKQHDYIIEFFDYTV----- 359  
348 ADVPEHFRGRVSIWAMVT--SVDSGQQ-----VAFDDSTPVQRQLVDIYISK 392  
360 -----LRPSLNFTATVKVTRADGNQLTLEBRNNWITVTQRYTEYWGSGNSGNQKMEA 414  
393 DTRKQKFGLAYVGVKLSVYDGSF-----AEGVTVOI-----KAEL 429  
415 VQKIN-YT---VPQSGTFKIEFFILEDSE---LQKAYELGSK-----SSMAVHSL 459  
430 TPKNITVTSVVSQRLVGVPEIPIPTSAOHVLETKVMALNGKPVGAQVLPYLSLGSW 489  
460 FKPSKTYIOLKTRDENIKGSPPELVVSGNKRILK-ELSYMVSRGOLVAVGRQ----- 512  
490 Y-SPSQCYLQPPSHPLQGEAYEYVSKTSCPCNFTLYVEVAARGNIVLSGQPAHTTQ 548  
513 -----NSTFSLTPNSWTPKACVIVYI 536  
549 QRSKRAAPALEKPIRLTHLSETEPPPAEABVDVCTSLHLAVTP--SMVPLGRLLVYV 606  
537 EDDEITSDVLKI PVQLVFNKIKLYSKVKAEPSEKVSIRISVTPDSITGVVAVDKSV 596  
607 RENEGVADSLQFAVEFFENQSVTSANETQGEVVDLIRIAR--GSCVCVAAVDKSV 665  
597 NLMAASNDITMENVHELELYNTG-----YVLGMFM 627  
666 YLLRSFGRLTPAQVFQELEDDYVSDSGVSGREDGPFWWAGLTQRRRSSVFPWPGITX 725  
628 NSPAVFOEGLWLTD-ANLTKVDIGVADNAEVAERFMEENEGHIVDIDHFLSGSSPH- 685  
726 DSGFAFTETGLVMDRVSJLNRQDGLY--TDEAVPAFQHTGSLV-----AVAFSRHP 778  
686 -----VRKHFPETWILDTNMGRYIYQ-BFEVTVPSDITSWVATGFEVISEDIGLGLTTT 738  
779 PRTEKRKXTPPETWIWHLNIDSPSGEGTLVKVPDSITSWGEAVALSTSQGLGT-AE 837  
739 PVELOAQOPFFIFNLPSYVIRGEPALEITIFNLYKDATEV--KVILEKSKDFDILMVS 796  
838 PSLKTKFPFVDFMPLAIRGEQVKIPUSVYNYMTGCAEVYKUSVPKGIQF----- 891  
797 SEINATGH-----QOTLLVPSEDCATVLPPIRTHLGEIPITVTLAS----- 838  
892 -----VGHGPKRHVTKMCAVPAEAPIMVWVLSFSLGLNITAKALAYGDTNCCRDGRS 946  
839 -----PTASDAVTQMLLVKAEGIEKYSQSIL----- 865  
947 SKHPEENHADRVRPIGVHDVRRSVYVWAEVGPRAITYTSAPFCPSERVHISTPNKYEFQVY 1006  
866 ---LDLT-----DNRL-----Q 874  
1007 QRPRLTRFVAVRAHNDARVALSSGQDGTAGMIEIVLGHQHTRSWISTSKXGEPVASA 1066  
875 STLKTLSP----- 882  
1067 HTAKILSDPEPTFWISWRGGGLIQVHGHPESNESIVAVTLPRPPEVQFIFSTGWGSM 1126  
883 -----SFPNTVTGSEVRQITAIAGDVLGPSINGLASLIRMPYGC 921

1127 GEFIRWKEVDESYSEAFITLGVPHGAIPGSEATASIIGDVMGPTLHNLNLRULRPFGC 1186  
922 GEQNNIFAPNIYILDYLTKKQLTDLNKEKALSFMRQGYQRELLYQREDFGSFAFNVD 981  
1187 GEQNNIHPAPNVFLVKYLQTKQLSPEVERETDYLAVQYQRLTYRQDGSYAFGERD 1246  
982 PSGSTWLSAFVLRPLEADPYIDIDQNLHRTYTWLKGHOKSNGCFWDPGRVHSELOGG 1041  
1247 ASGSMWLTAFVLSKFAQARSEFIVDPRELAASKWIIQQOQADGSLAVORVNLKNDIOGG 1306  
1042 NKSPVTLTAYITVTSIL--GYRKYQPNIDVOESIHFLESEFSRGISDNVTALITIALYSSV 1099  
1307 IHGIVPLTAYVVVALLETGTASEERSTDKARHFLSESAAPLAM-DPYSICALITYALTLL 1365  
1100 GSPKAKEALNMLTWRAEQEGMQFVWSSESXLSQSWQPR-----SLDIE 1143  
1366 RSPAPEALRKLRSILAIMRDGVTHW-----SLNSWDVDKGTFLSFDVSVSQSVSAEVE 1420  
1144 VAAVALLSHFLOFTSECIPIMRWLSRBNLSLGGFASTODTTVALKALSEPAAL----- 1197  
1421 MTAVALLTYTLGDDVAALPVVKWLSQORNALGGFSTQDTCVALQALAEVALLSYAGGI 1480  
1198 -----MNTERTNIQVTVTG--PSSPSPLAVVQPMVNI SANGFGFAICQ 1239  
1481 NLTVSLASTNLDYQETPELHRTNOKVLQTAAPSLTGLTFV-----SAKGDGCLMQ 1532  
1240 LNVTVNVK--ASGSSRRRRSIQOE-----APDLDVAVKENK 1274  
1533 IDVTYVDPVPAKFAFQLLVLSLOPFEAQGRPPMPASAAEGSRGDWPFADDDPAADQHH 1592  
1275 DDLNHDVLNVCTSFSGPQRSGMALMEVNLISGFMVPSAISLSST-----VKKVEYDH 1327  
1593 QEYK-VMEVETRWLHAGSSNMAVLEVPLLSGFRADIE--SLEQLLLDKMGMKRYEVAG 1649  
1328 GKLNLYLDSV-NEQFCVNIPAVNFVKNSTQDASVIVDYIEPRROAVRSYSEV----- 1382  
1650 RRVLYFDEIPSRCLTCVFRALRECVVGRTSALPVSYDYIEPAFEATFRFYNVTHSPL 1709  
1383 --KLSDDLCDSDVQ-----GCRPCEDGASGSHHSSVI 1413  
1710 ARELCGAPACNEVERAPARGCFWPFSGGPAVAPBEGNAI 1749

## RESULT 10

US-09-972-211-69

Sequence 69, Application US/09972211

Publication No. US20040048245A1

GENERAL INFORMATION:

APPLICANT: Shimkets, Richard A

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Burgess, Catherine E

APPLICANT: Zerhusen, Bryan D

APPLICANT: Mezes, Peter S

APPLICANT: Rastelli, Luca

APPLICANT: Malyankar, Uriel M

APPLICANT: Grosse, William M

APPLICANT: Alsobrook II, John P

APPLICANT: Lepley, Denise M

APPLICANT: Spytek, Kimberly Ann

APPLICANT: Li, Li

APPLICANT: Edinger, Shlomit

APPLICANT: Gerlach, Valerie

APPLICANT: Ellerman, Karen

APPLICANT: MacDougall, John R

APPLICANT: Gunther, Erik

APPLICANT: Millet, Isabelle

APPLICANT: Stone, David J

APPLICANT: Smithson, Glenda

APPLICANT: Szekeres Jr, Edward S

TITLE OF INVENTION: No. US20040048245A1 Human Proteins, Polynucleotides Encoding The

TITLE OF INVENTION: Methods Of Using The Same

FILE REFERENCE: 21402-141

```

; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 69
; LENGTH: 1476
; TYPE: PR1
; ORGANISM: Cavia porcellus
; US-09-972-211-69

Query Match      20.3%; Score 1491; DB 12; Length 1476;
Best Local Similarity 28.8%; Pred. No. 1.1e-112;
Matches 451; Conservative 292; Mismatches 524; Indels 300; Gaps 60;

QY 4 PPLTAAHLVCVTAALAVAPGRFLVTPAGTIRPGCVNVTIGVLELHCPQVTVKABL- 62
D 11 PVLL-----LLLLAADAASISGKQYMYLPSLLHSGTPEKICL-LLTQLNETVTVKASLD 65
QY 63 -LKTASNLTVLEAEQVPEKSGFKTLTLPSSLNPSADEIYELRVTRGTQDEILFNSNR 121
D 66 TIRENSLFNMVAEKDLFCVAF---TVQSPYPEAVMFLTVVEGPTHG---FRSRKT 119
QY 122 LSPETKRISVFIQTDKALYKQKQVPRVITLPSDFKPYKTSLN-----ILIKDPKSNLI 176
D 120 VLVKSKDSLVEFQTDKPIYKPGQTVKARVVSLDENFRP-----LNELFPFLIFIQDPKGNRV 175
QY 177 QWLISOQSDLGVLISKVTFQLSHPIILGDWSLQV-QVNDQTYQSFQVSEVULPKFVTLQT 235
D 176 MOWNLKLERGLTQLSPFLSEPLLGSYVVVHKGSGRHHHSFTVEEFVLPKPFQVQSM 235
QY 236 PLVCSNMSKHLNGTITAKTYGPKVKGVDVLTLEL-----PLSFWKKKNIKTFF---KING 288
D 236 PKXITILEQEFVTVSGRYTYGKVPNGNITMSICRNVNPSACLSE---SRAFCCKYQ 292
QY 289 SAN-----FQFNDEEMK-----NVDSSNGLSEYLDLSPGPFVEILTTVT 328
D 293 QLSNQGCFIQOVKTNDQFLRKEVEMLRVEAKIREEGTG---VQLTGTGFSEITATIT 348
QY 329 ESVTGISRNVTNFFQKHDIYIEFFDYTVLAKPSLNFTATVKVTRADGNQLTLEERRNN 388
D 349 K-----LSFVKVDSYVRPGVFFQGVRL--VDGKNVMPHXM-- 383
QY 389 VVITVQRYNTEYWSNSGNQKQMEAVQ-KINTVFPQSGFKIEFFILEDSS-----ELQ 443
D 384 ITITASEANY-----HSNATTDEGLVQFSINTTNMIGTSLNIQVKKHDKSTNCYQWLL 438
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Qy 1374 AVRSYNS 1380  
Db 1461 AIAEYHA 1467

US-10-096-625-69  
Query Match 20.3%; Score 1491; DB 12; Length 1476;  
Best Local Similarity 28.8%; Pred. No. 1.1e-112;  
Matches 451; Conservative 292; Mismatches 524; Indels 300; Gaps 60;

RESULT 11  
US-10-096-625-69  
Sequence 69, Application US/10096625  
Publication No. US20040068095A1  
GENERAL INFORMATION:  
APPLICANT: Shinkets, Richard A  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Mestes, Peter S  
APPLICANT: Rastelli, Luca  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Grosse, William M  
APPLICANT: Alsobrook II, John P  
APPLICANT: Lepley, Denise M  
APPLICANT: Spytek, Kimberly Ann  
APPLICANT: Li, Li  
APPLICANT: Edinger, Shlomit  
APPLICANT: Gerlach, Valerie  
APPLICANT: Ellerman, Karen  
APPLICANT: MacDougall, John R  
APPLICANT: Gunther, Erik  
APPLICANT: Millet, Isabelle  
APPLICANT: Stone, David J  
APPLICANT: Smithson, Glenda  
APPLICANT: Szekeres Jr, Edward S  
APPLICANT: Ji, Weizhen

TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding Th  
TITLE OF INVENTION: Methods Of Using The Same  
FILE REFERENCE: 21402-141 CIP  
CURRENT APPLICATION NUMBER: US/10/096,625  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: 09/972,211  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 60/238,325  
PRIOR FILING DATE: 2000-10-05  
PRIOR APPLICATION NUMBER: 60/238,323  
PRIOR FILING DATE: 2000-10-05  
PRIOR APPLICATION NUMBER: 60/238,400  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,397  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,401  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,379  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,402  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,384  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,373  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,372  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,383  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,382  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/275,892  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/296,860  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 200  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 69  
LENGTH: 1476  
TYPE: PRT  
ORGANISM: Cavia porcellus

Qy 4 PPLTAHLLCVCTAALAVAPPRFLYTAFCIIPGNGNVTIGVLELHCHSFQVTVKAEI- 62  
Db 11 FVLL-----LLTLLAADASISGKQPMVVLPSLLHSGTPEKICL-LLTQLNETVTVKASLD 65  
Qy 63 -LKTASNLTVSVLEAEGVFEKGSFKTLTLPSPILNSADEIYELRVGTGRTODELFSNSTR 121  
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Qy 122 LSFETKRISVFIOTDKALYKPKQEVKFRIVTLPSDFPKYKTSLN-----LLIKDPKSNLI 176  
Db 120 VLKSKDSLAVFVQTDKPIYKPGQTVKARVSLDENFRP-----LNELPFLIFIQDPKGNRV 175  
Qy 177 QOWLSQQSDGLGVISKTQLSHPILGDSIOV-OVNDQTYVQSFQSVYVLPKFEVTLQOT 235  
Db 176 MQWNLKLERGLTQLSPLESPELGSYVVVHKESGGRMHHSFTVEFVLPKFEVQVSM 235  
Qy 236 PLYCSMSKHLNGTITAKYTYGKPVKGDVTLTFL-----PLSFWKKKNIKTTF--KING 288  
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Qy 289 SAN-----FSNDEBK-----NWDSSNGLSEYLDLSSGCPVEILTIT 328  
Db 293 QLNQGGCFIOQVKTNDPQLRREKEYEMLRVEAKIREEGTG-----VQUTGTGFSBITAIT 348  
Qy 329 ESVTGISRNVSTNVFFKQHDYIIIEFFDYTYTVLKPSLNFATATKVTTRADGNQLTLEERN 388  
Db 349 K-----LSFVKDVSIVRPGVPFGQVRL--VDGNVPMPHKM-- 383  
Qy 389 VVITVQRNYTEYWSGNSGNQKQEAQV-KINYTVQSGTFKIEFPLEDESS-----ELQL 443  
Db 384 ITITASEANY-----HGNATTDENGLVQFSINTNMIGTSLNQVHKHDKSTCNDYQWLL 438  
Qy 444 KAYFLGSKSSMAVHSLPKSPKTYIQLKT-----RDENIKVGSPPFELVSVGNKELKE 495  
Db 439 EANECASTANAVESL-----SRSFVHLEPQLGKLPCHQOTQTFKA---HVLKG-QELKE 489  
Qy 496 L--SYMVSRGQLVAVG-----KQNST---MPSLTPENSWTPKACVIVYVIBDDGEII 543  
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Qy 632 VFQECGLWLTDLNLTXYIDGVYDNAEYAFRFEENEHGHIVDHDPSLSSH----- 685  
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Qy 837 LSPT--ASDAVTOMILVKAEGIEKYSQSILDLTDNRLOSTLTKTLFSFPNVTGSR 894  
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Db 442 EEAHTAY-----LVFSPKSFVHLEPMSHELPCGHTQTQVQAHYILNGTLLG 489  
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QY 897 ITAIGDVLGFSINGLASLIMPYGCGEQNMNFAPNIYLDYLTKKQKLTDLNKEALSF 956  
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QY 1223 ----PMAVNTSANGFGPAICQLAVNVNVKASGSSRRRSIQNCEAFDLDVAVK---ENK 1275  
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QY 1276 DLN-HVDLNVCTSPSGP-----RSGMALMEVNLISGFMVSEAI SL---SETVKVEYDHG 1328  
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Db 1414 HVLIYLDKVSNTLSLFTTQVDFVRDLKPAIVKVDYIYETGEFALAEYNA 1465

US-10-096-625-65  
; Sequence 65, Application US/10096625  
; Publication No. US20040068095A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Zernusen, Bryan D  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsbrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Spytek, Kimberly Ann  
; APPLICANT: Li, Li  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John R  
; APPLICANT: Gunther, Erik  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David J  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Szekeres Jr, Edward S  
; APPLICANT: Ji, Weizhen  
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding The  
; FILE REFERENCE: 21402-141 CIP  
; CURRENT APPLICATION NUMBER: US/10/096,625  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 09/972,211  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/238,325  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,323  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,400  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,397  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,401  
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; PRIOR APPLICATION NUMBER: 60/238,379  
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; PRIOR APPLICATION NUMBER: 60/238,402  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 30/238,384  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,373  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,372  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,383  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,382  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/275,892  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/296,860  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 1474  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-096-625-65

Query Match 19.6%; Score 1441; DB 12; Length 1474;  
Best Local Similarity 29.2%; Pred. No. 1.5e-106;  
Matches 453; Conservative 264; Mismatches 551; Indels 284; Gaps 60;



Db 125 EDSLIVFQTDKSIYKPGQTVKRVVMDENFHPNELIPLVYIQDPKGNRIQWQSFQLE 184  
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Db 185 GGLKQSFPLSSPFPQSGYKVVVQKSGGRTEH-PFTVEFVLKPEVQVTPKIIITILE 243  
Qy 244 KHLNGTITAKYTKGPKVKGVDVTLFPL-----SFWGK 276  
Db 244 EEMNVSCGLTYTKGPKVGHVTVSICRKYSDASDCHGEDSQAFCEKFSQOLNSHGCFYQO 303  
Qy 277 KGNITKFKNGANFENDEEMKNVMDSSNGLSEYLDLSSPGVRIILT-----TVTESV 331  
Db 304 VK--TKVQLK-----KEYEK-----LHTEAQIOEGTVVELTGROSSEITRI 347  
Qy 332 TGISRNVTNVFKQHDYIIEPFDYTVLKPNSLNFATVKTADAGNQLTLEBRRNVVI 391  
Db 348 TKLS-FVKVDSPFRQ--IPFFG-----QVRLVDGKGVPIP-----NKVI 384  
Qy 392 TVTORNVTWYSGNSGNQKMEAVO-KINYT--VPOSGTFKIEFP-----TLEDS 438  
Db 385 FI-RCNEANY--SNATDDEGLVQPSINTINMGTSITLVVNYKDRSPCYGQWVSEEH 441  
Qy 439 SEQLKAYF-GSKSSMAVHSLFKSPKTYIQLTRDENIKVGS-----PELVVSGNK--R 492  
Db 442 EEAHTAY-----LVFSPKSFVHLEPMSHELPCGHTQTQVQAHYILNGGTLG 489  
Qy 493 LKELS--YMVVSRQOLVAVG-----KONST-----MFLTPENSWTPKACVIVYIEDG 540  
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Qy 632 VFJECGLWLTDLNLTVDYIDGVYDNE-----YAEFMEENEHIVDIDHFL 680  
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Db 1414 HVLIVLDKVSNTLSLFTVLQDVPVRDLKPAIVKVYDYETDEFAIAEYNA 1465

## RESULT 15

US-10-052-817-2  
; Sequence 2, Application US/10052817  
; Publication No. US20020114792A1  
; GENERAL INFORMATION:  
; APPLICANT: Tanzi, Rudolph E.  
; APPLICANT: Kovacs, Dora  
; APPLICANT: Saunders, Aleister J.  
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for  
; TITLE OF INVENTION: Alzheimer's Disease  
; FILE REFERENCE: 0609.4460005  
; CURRENT APPLICATION NUMBER: US/10/052.817  
; CURRENT FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: 09/241,606  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: 09/148,503  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 60/093,297  
; PRIOR FILING DATE: 1998-07-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1474  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-052-817-2

Query Match 19.6%; Score 1441; DB 13; Length 1474;  
Best Local Similarity 29.1%; Pred. No. 1.5e-108;  
Matches 451; Conservative 266; Mismatches 551; Indels 284; Gaps 59;

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QY 277 KNIITKTFFKINGANFENDEEMKVMNDSSNGLSLEYLDLSSPGPBEILT-----TVTESV 331  
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QY 392 TVTORNYTEYSGNSGNQKWEAVO-KINYT--VPOSGTEPKIEFP-----LLEDS 438  
Db 385 FI-KGNEANYI--SNATTDHGLVQPSINTNVNGTSLTVRVNYKORSPCYGYQWVSEBH 441  
QY 439 SEIQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS----PFEVLVSGNK--R 492  
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QY 1125 VSSSEKLSDSWQPR--SLDIEVAAYALLSHFLOFO---TSEGIP-----IMRWLSQRNSL 1175  
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Job time : 65 secs

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Run on: August 10, 2004, 19:25:04 ; Search time 23 Seconds  
(without alignments)  
3205.299 Million cell updates/sec

Title: US-10-020-095-4  
Perfect score: 7348  
Sequence: 1 MQGPPL2TAHLLCVCTAL.....HSSVIFPCFKLLYFMELWL 1428

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	19.6	1474	4	US-09-241-606-2
2	973.5	13.2	1651	1	US-08-447-411-2
3	931	12.7	1663	2	US-08-793-126-1
4	931	12.7	1663	3	US-09-132-271-1
5	931	12.7	1663	3	US-09-142-334-22
6	921	12.5	1676	4	US-08-487-283A-2
7	894	12.2	1642	2	US-08-662-227-2
8	894	12.2	1642	4	US-09-017-947-2
9	894	12.2	1642	4	US-09-925-442-2
10	885	12.0	1642	1	US-08-447-411-45
11	880	12.0	1648	2	US-08-662-227-35
12	880	12.0	1648	4	US-09-017-947-35
13	880	12.0	1648	4	US-09-925-442-35
14	768.5	10.5	1333	1	US-08-447-411-76
15	758.5	10.3	1333	2	US-08-662-227-34
16	758.5	10.3	1333	4	US-09-017-947-34
17	758.5	10.3	1333	4	US-09-925-442-34
18	329	4.5	645	1	US-07-779-172A-3
19	271	3.7	1667	4	US-09-489-039A-11624
20	234	3.2	113	4	US-09-311-352B-2
21	215.5	2.9	250	4	US-09-241-606-4
22	211.5	2.9	1716	4	US-09-543-681A-7609
23	185	2.5	183	4	US-09-311-352B-4
24	185	2.5	2385	4	US-09-543-681A-6304
25	180	2.4	1341	4	US-09-252-991A-26785
26	177.5	2.4	2777	4	US-09-543-681A-6124
27	174.5	2.4	2366	1	US-08-480-604A-10

28	174.5	2.4	2366	2	US-08-405-496A-10
29	174.5	2.4	2366	3	US-08-915-136-10
30	174.5	2.4	2366	4	US-08-957-310-10
31	174.5	2.4	2366	4	US-10-011-366-10
32	174.5	2.4	2366	4	US-09-084-517-10
33	171	2.3	3290	4	US-09-328-352-5486
34	165	2.2	2037	4	US-09-543-681A-5538
35	161	2.2	2199	4	US-08-793-273C-2
36	161	2.2	2199	5	PCT-US95-11684-2
37	160.5	2.2	403	1	US-08-118-674-1
38	157.5	2.1	2200	4	US-09-796-575-2
39	156	2.1	10182	4	US-09-134-001C-3159
40	153.5	2.1	3169	4	US-09-453-702B-257
41	152.5	2.1	1095	4	US-09-206-942-69
42	152.5	2.1	1536	1	US-08-038-682-2
43	152.5	2.1	1536	1	US-08-302-832-2
44	152.5	2.1	1536	2	US-08-530-198-2
45	152.5	2.1	1536	2	US-08-469-880-2

## ALIGNMENTS

RESULT 1  
US-09-241-606-2  
; Sequence 2, Application US/09241606  
; Patent No. 6472140  
; GENERAL INFORMATION:  
; APPLICANT: Tanzi, Rudolph E.  
; APPLICANT: Kovacs, Dora  
; APPLICANT: Saunders, Aleister J.  
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for  
; TITLE OF INVENTION: Alzheimer's Disease  
; FILE REFERENCE: 0609.4460003  
; CURRENT APPLICATION NUMBER: US/09/241.606  
; CURRENT FILING DATE: 1999-02-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1474  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-241-606-2

Query Match		19.6%	Score 1441, DB 4, Length 1474;
Best Local Similarity		29.1%	Pred. No. 7.7e-111;
Matches 451;		Conservative 266;	Mismatches 551; Indels 284; Gaps 59;
QY	12	LLCCTAALAVAGPRFLVTPAGIIRPGNVTIGVELLEHCPQSVTVKAEILLKTASLTV	71
DB	15	LLVLLPTDASVSGRPQYMLVPSLLHT-ETTEKCVLLSYLNETVTVSASLESYRGNRSL	73
QY	72	-SVLEAEG-VPEKGSFKTLTLPSPILNSADP---IYELRVTRGTODEILPNSNTRLSGET	126
DB	74	FTDLEANDVLHCVAF-----AVPKSSNEEVFLTVQVKGPTQE---FKKRTTVMVKN	124
QY	127	KRISVFIOTDALKYKPKQEVKFRIVTLFSDPKPKYKTSNLIL-INKPKSNLIQOQLSQSD	185
DB	125	EDSLVFVQTDKSIYKPGQTVKFRVVSMDENPHNLPLIPLVYIQDPKGNRIAQWQSFOL	184
QY	186	LGVLSTKTFQLSHSHILGDWSIQOVND--QTVYQSFOVSEYVLKFEFTVLTPLYCSMNS	243
DB	185	GGLQKQFSLSEBFFQGSYKVVVQKSGGRTEH-PFTVEEFVLKFEVQVTVPKIITILE	243
QY	244	KHLNGTITAKTYGKPKYKGVDTLTLFLPL-----SFWGK	276
DB	244	EEMNVSVGLTYGKPVPGHVTVSICRKYSDASDHGDSQAFCEKFSQGLNSHGCFVQ	303
QY	277	KXNTKFKINGSANFNSFNDDEEMQNVMDSSNGLSEYLDLSPGPEVILT-----TVTESV	331
DB	304	VK--TKVFQLXR-----KEYEMK-----LHTEAQIQEGTVELTGQSSSEITRTI	347
QY	332	TGISRNVTSTNVFFKHQDVIIEFFDYTTVLKPSLNFATKTVKTRADGNQLTLEERNRWI	391

Db 348 TKLS-FVKVDSHFRQG--IPFFG-----QVRLVDGKGVPIP-----NKVI 384  
Qy 392 TVTQBNYTEWSSNSGNOXKQWAVO-KINYT--VPOSGTFKIEBP-----ILED5 438  
Db 385 FI-RGNEANY--SNATTDHGLVQFSINTNVGTSLVTVVNYKDRSPCYGQWVSEEH 441  
Qy 439 SEQLKAYFLGKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS-----PPELVVSGNK--R 492  
Db 442 EEAHTAY-----LVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGTLLG 489  
Qy 493 LKELS--YMWVSGQLVAVG-----KONST-----MPSLTPENSWTPKACVIVYIEDDG 540  
Db 490 LKLSFYLLIMAKGIVRTGHLGLLKQEDMKGHFISIPVKSIDIAPVARLLIYVLPTG 549  
Qy 541 EITSVLKIPVOLVFNKIKLYKSKVKAEPSEKVSIRISVTQDSTVIGIVAVDKSVNLWN 600  
Db 550 DVGDSAKYDVENCLANKVDLSFSPQSPLASHAHLVTA--POSVALRAVDOSVLLMK 608  
Qy 601 ASNDITMENVHEL-ELYNTGY-----YLGFMFMS-----FA 631  
Db 609 PDAELSASSVNLPEKDLGFGPLNDQDEDCINRHNVIYINGITYTVPVSTNEKDMYS 668  
Qy 632 VFCEGLVWLTANDLTIDYIDGVYDNAB-----YAEFMEENEGHIVDIDHDFSL 680  
Db 669 FLEDMGUKAFTNSKIRPKPKPCQLOQVEMHGPGLRGVFPYSDVMGRGHARLVHVE-- 725  
Qy 681 GSSPH---VRKHFPETWILDTMNGYRIYQEFVTVPSDITSWVATGFWISEDGLGLTT 737  
Db 726 ---PHTETVKYRPETWILVNVNSAGVAEVTVPDITTEWKAGAFCLSEADAGLIGSS 782  
Qy 738 TPVELQAFQFFFLNLPYVIRGEPEALEITTFNYLKDATEVKVILEKSDKFDILMTSS 797  
Db 783 T-ASLRAFQFFVELTWPYVIRGEAFTLKATVNLVLPKCIKIRVSVQLEASPAFLVPEBK 841  
Qy 798 E-----INATGHOQTLLVPSEGDATLFPFIRPHLGEIPITVITALS-----PTA 841  
Db 842 EQAPHCICANGRO-----TVSWAVTPKSLGNVNFVTSAALESQELCGTEVPSV 890  
Qy 842 ---SDAVTQMLVKAEGTEKYSQSLDLDNRLQSTLKSFPFPNTVTGSRVQ 896  
Db 891 PEHGRKDTVIKPLIVEPEGLEKETTFNSLLCPGSGEVS---EELSCLKPPNVVVEASARAS 947  
Qy 897 ITATGDLVGLSINGLASLIMPYCGGONMINFAPNIYILDYTKKQLTNDLKERALGF 956  
Db 948 VSLGDLGSAWQNTQNLQPTGCGEQNMVLFPAPNIYLDYNETQQLTPEIKSKAIGY 1007  
Qy 957 MRQGYORELLYQREDGFSAFG-NYDPS-GSTWLSAFVLCFLEADPYIDIDQNLHRTY 1014  
Db 1008 LNTGYQRLNKHVDGYSYTFGERYGRNQNTWLTAFVLKTAQARAYIFIDEAHITQAL 1067  
Qy 1015 TWLKGHOKSGEFPDPRVHSELOGGNKSPVLTAYIVTSLGGRKYQENIDVQESSIH 1074  
Db 1068 IWLQKQKNGCFRSGSLNNAIKGGEDEVLTSAVITIALLEIPLTVTHVPRVNRALFC 1127  
Qy 1075 LES-----BPSRGISDNYLTALITYALSSVGS--PKAKEALNMLTWRAEOEGMGQFW--- 1124  
Db 1128 LESAWKTAQEGDHG--SHVYTKALLAYAFALAGNQDKEVLSLNEAEVKKDMSVHWERP 1186  
Qy 1125 VSSSKLSDSQWPR--SLDTEVAAYALLSHFLQF---TSEGIP-----IWRWLSROENSL 1175  
Db 1187 QKPAPYGHFPEOAPSAEEMTSYVLLA--YLTAQAPTSSEDTSATNIVKWKITQOQNAQ 1245  
Qy 1176 GGFASOTDTTVALKALSEFAALMNTERTNIQVTVTGSPSPSLAVQO----- 1222  
Db 1246 GGFESTQDTTVALHALSKYGAFT-RTGKAAQVTIQSSCTFSSKQVQDNNELLQQVS 1304  
Qy 1223 ---PMAVNTSANGFGFAICOLNVVNVKASGSSRRRSRSTONQAFDLDVAVK---ENKD 1275  
Db 1305 LPPELPGYSMKVTGEGCVYLTQSLKYN-----LPEKEEFPFALGVQTLFQTC 1353  
Qy 1276 DLN-HVDLNVCTSFSGPG---RSQWALMEVNLISGFMPVPEASLSL---SETVKVKEVDHG 1328

Db 1354 EPKAKTSFQISLSVSYTGSRSSASNAIVDMVMSGFTPLKPTVKMLERSHVRTEVSSN 1413  
Qy 1329 KLNLYDSVNETQFCVNIPAVRNEKVSNTQDASVSIVDYIEPRRQAVRSYNS 1380  
Db 1414 HVLIVLKVSNQTLISLFTFVLQDVPVRDLKPAIVKVVDYVETDEFAIAEYNA 1465  
RESULT 2  
US-08-447-411-2  
; Sequence 2, Application US/08447411  
; Patent No. 5773243  
; GENERAL INFORMATION:  
; APPLICANT: FRIZINGER, DAVID C.  
; APPLICANT: BREDEHORST, REINHARD  
; APPLICANT: VOGEL, CARL-WILHELM  
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,411  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/043,747  
; FILING DATE: 07-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5773243man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-101-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1651 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-447-411-2  
Query Match 13.2%; Score 973.5; DB 1; Length 1651;  
Best Local Similarity 23.5%; Fred. No. 1.2e-71;  
Matches 391; Conservative 278; Mismatches 649; Indels 343; Gaps 61;  
Qy 1 MQGPPLLTAAHLICVCTAALAVAPGPRFLVTPAGIIRPGNVITIGVELL-EHCPSQVTVK 59  
Db 1 MEGHALYVLAALLIGFPGS---SHGALVTLITPAVLATDTEQILVEAHGDSGTPKSLDIF 57  
Qy 60 A-----ELLKTKASNLTVSVLEAGVFEKSGFKTLILPSLPLNSADEIYELRVGTQDEIL 115  
Db 58 VHDFFPRKQKTLFQSRVDMNQAGSMFVT---PTIKVPAKELNKSKQNVVVKVVGQVA 114  
Qy 116 TSNRSLSFETKRIKSVFTQTDKALYKPKQEVKFRIVTLFSDFKPKYKSLNLIKDKPSNL 175  
Db 115 LEKVLLSYQSG--FVFIQTDKGIYTPGSPVRYRFSV--DHNHMRMDKTIVE----- 164  
Qy 176 IQQWLSQQSDIGVSKTKTQLSSHP-----LGDWSIQVQVN---DQTY 216  
Db 165 -----FQTPGIV-----VSKPVPNSGSIIRPNLPVLSFGTWKAVAKYEHSPESY 213

QY 217 QSQVSEYVLPKFEVTLQTP---LYCSMKSXHLNGITAKYTYGKPVKGDTLTLFLPLSF 273  
Db 214 AYDVEYVLPSEVRLQPSDKFLYIDGN-KNFHVSITARYLYGKVEG-VAFVPGVKI 271  
QY 274 WGGKXNI---TKTFKINGSANFNDDEEMKNVMSNGLSEYLDLSLSPGPVEIITVTTE 329  
Db 272 DDAKKSIPDSLTRIPIIDGGEATLRDLRSRFDQLNQLVGHLYVS-----VTVITE 325  
QY 330 SVTGISRNVSTNVFFKQHDYIIEPPDYTVVLPKSLNFTATVKVTRADGNQLTLBERNNV 389  
Db 326 SGSDMVVTEGGHIVTSPQIYFTKPKYFKGMPYELTVYVTPDGPAA-----H 378  
QY 390 VIIVTQRTNTEYSGNSGNQKMEAVQKINYTP---QSGTFKIEPPILEDSESLQKAY 446  
Db 379 VPVSEAIHSE-----GTTLSGDTAKULNPLNIQS-----LPIITVRNHGDLPE 425  
QY 447 FLGSKSMVAHSLFKPSKTYIOLKTRDENIKVGS--PFELVVSNG-----KELKELSYNV 500  
Db 426 RQAIKSNATAYQTQGSSENYLVAITSTEIKPGDNLVFNFNVRGNANSLNIQKTYLI 485  
QY 501 VSRGQLVAVGK-----QNSTMFSLTPENSWTPKACVIVVYIEDDGEIISDLVKIPVQ-- 552  
Db 486 LNKGIKFKVGRQPRRQGNLVTWNLHITPDLPSFRVAYQVGNNEIVADSVVDVDKT 545  
QY 553 -----LVFK-----NKKLYMSKVKAEPSEKVSRLISVTPQDSIVGIVADVXSNLMMAS 602  
Db 546 CMGTLLVVKGASSDRIO-----KPGAAMKILE-GDPGARVLVAVDZAVVYVLDK 596  
QY 603 NDIITMENVHELYNTGYVLGMFMSPAVFOCGLWLTDLNLT----- 647  
Db 597 YKISOAKIWDITKSDFGCTAGGQNNLGVFEDAGJALTSTNLTNFKQSAKCPQANR 656  
QY 648 -----KDYIDGVVDN-----AEYAEFMEENEG----- 670  
Db 657 RRRSSVLLDLSKASKAAQFQDQGLRKCCEGDGHENPMGVTCEKRAKVIQEGDACKAAFL 716  
QY 671 --HIV-----DIHDSFGSPHV-RKHFPETWL-----DTNMG 702  
Db 717 CCHYKIGIRDENQRESELFLARSDFEDELFGDDNIISRSDFPESLWLTTELTGEPNQG 776  
QY 703 YRIQEFVETVP---DSITSWATGVFVISEDGLGLTTT-----PVELQAFPPFFIF 751  
Db 777 IS-----SKTVPYLRDSITW-----ELLAVGLSPTKICVAEPYEITVMKDFDID 823  
QY 752 LNPYSVIRGEEPALEITIPNLUKDATEVVKVIEKSKDFILMTSSEINATGHQOQLLVP 811  
Db 824 LRLPYSVVKNQVEIRAILLYNADEDIYVRVELIYNPAF-----CSASTEGQYRQFPK 879  
QY 812 SEDGATVLPPIRTHLG--EIPITVLTASDAVTQMLVKAEGIEKYSQSILLDLT 869  
Db 880 ALSRAVPFVIVPLEQGLHDEVIASVRGELASDGVKRLKVVPEGERKNIVITIELDPS 939  
QY 870 DNRLOST--LKTLSFSPPPNTVTGSERVQITAGD---VLGPSING--LASLIRPYGC 921  
Db 940 VKGVGGTQELTVIANKLDKVPDTEVETRISVLGDPVAQIENSIDGSKLNHLIITPSC 999  
QY 922 GEQNMINFANI---YILDYLTKKQLTDLNKEKALSPRQGYORELLYQREGDGSFARG 978  
Db 1000 GEQNMIMTFSVATYLDATQWENLGVDRTEAIKQIMTGVAQOMVYKKAADHSYAAT 1059  
QY 979 NYDPSSGTLWSAFVLCFLEADPYI-DIQONVLRHTYTWL-KGHQKSNGEFWDPCGRVHS 1036  
Db 1060 N--RASSWLTAYVVKVLASANMVKDISHEIICGGVKVLLNLRQOPDGVFKENAPVING 1117  
QY 1037 ELOGGNKS---PVTLYAVIVTSLLGVKYPQNPIDVOESIHFLSEFSRG-----I 1083  
Db 1118 EMLGGTKGAPFASLTAFIVTALLERSV-----CKEQINLDSINKATDYLKKYKYL 1172  
QY 1084 SDNYTLALITYALSSVSPKAEALNLTWRAEQEGMQFWSSESLSKSDSQPSRLDIE 1143  
Db 1173 QRYTTLTAYALA-----AARLNDRLVMAASTGRNRW-----EYNARTHNIE 1218  
QY 1144 VAAVALLSHFLOPQTSEBIPINRSLWRQNSLGGFASDTQDTVALKALSEFAALMNTER- 1202

Db 1219 GTSVALLALLKKKFAEVPVVRWMLIDQKYYGGYGTQATVWVFOALAEVEIQMPTHQD 1278  
QY 1203 TNIQVTVTPSPSP-----LAVQPMV-----NISANGFGFAICQLNVVNVK 1247  
Db 1279 LNLDSIKLPERVEPERSYINRNVQARTVETKLNEDEFTVSASGDGKATWLTILTVYNAQ 1338  
QY 1248 ASGSSRRRSIQNQEAPDLVAV-----KENKDDLHNVDLNVCTSFSGPGRSGMALME 1300  
Db 1339 L-----REDANVCK--FHLDSVENVELNLKQAGGKAALRLKICTRYLGEVDSTWTLID 1392  
QY 1301 VNLSGFMVPEAI-----SLSETVKVYVDH-----GKLNLYLDSVNETO-FCWNIPAV 1349  
Db 1393 ISMLTGPDPDAEDLKRLSNGVDRIYSKFEIDNNMAQKGTVVYLDKVSSEDECLHFKIH 1452  
QY 1350 RNFKVSNTODASVSIYDYEPQRCAVRSYSEVLSKSDCLSDVQGCPCDGDGSGSHH 1409  
Db 1453 KHFEVGTIOPGSVKVYSYINLDEQCTKPYHPDKETGLNKLKICHGNIORCAEETCSLLNQ 1512  
QY 1410 -----SSVIFIFCFKLL-----YFMEL 1426  
Db 1513 KKIDQLRIQKACQNVVDYVYTKLLRIEERKDGNDIYFMDV 1553  
RESULT 3  
US-08-793-126-1  
; Sequence 1, Application US/08793126  
; Patent No. 5849297  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Richard Alexander  
; APPLICANT: Farries, Charles Timothy  
; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE AND DORR LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: United States of America  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,126  
; FILING DATE: 07-FEB-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Hollie L.  
; REGISTRATION NUMBER: 31,321  
; REFERENCE/DOCKET NUMBER: 102286.377  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1663 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-793-126-1  
Query Match 12.7%; Score 931; DB 2; Length 1663;  
Best Local Similarity 23.0%; Pred.No.4.5e-68;  
Matches 376; Conservative 286; Mismatches 615; Indels 356; Gaps 62;  
QY 3 GPPIITAAHILCVCTALAVAPGRFLVTAPIIR-----PGNVTIGVELL 49  
Db 6 GPSLL-----LULLTHLPLALG-SPWYSITINILRLESETWVLEAHDAGQDVPVTVH 60





Best Local Similarity 23.0%; Pred. No. 4.5e-68;  
Matches 376; Conservative 286; Mismatches 615; Indels 356; Gaps 62;

QY 3 GPELLTAHLLCVCTAALVAPGRFLVTPAGIIR-----PGGNVTIGVELL 49  
DB 6 GPSLL-----LLLLTHLPLALG-SPMYSIITFNILRLESEBETVLEAHDAGDVPVTVVH 60  
QY 50 EH-----CPSQVTVKAEKLTASNTVSV-LBAEGVFEKGFSTLTLSPLNSADEIY 102  
DB 61 DFGKLVLSSEKVLTPATNHNHGNVFTIPANREFKSEKGRNKFVQA--TFGTQVV 117  
QY 103 ELAVTGRTOEILFNSSTRLSFETKRIISVFIOQDKALYKPKQVKEPRIVTLFSDFKPYKT 162  
DB 118 EKVVLSLQSGYL-----FIQDKTIYTPGSTVLYRIFTVNHKLLPVGR 161  
QY 163 SLNLIKPKSNLIQ-WLSQQSDLGVIKTFQSLSHPILDGWSIOVQND---QTYIOS 218  
DB 162 TVMVNIENPGIPVKQDLSLSSQNLGVLPLSWDIPELVNMGWKIRAYENSPPQVFSTE 221  
QY 219 FOYSEVLPKFEVTLQ--TPLYCSMSKHLNGITAKYTYKPKVKGDVTLTF-----268  
DB 222 FEVKEYVLPSEFVIEVETEFYIYNEKLEVTITITARFLYKXVGTATFVIGIQDGEOR 281  
QY 269 -----LPLSFWGKKKNIITFKINGSANFSFNDEEMKNVMSNGLSEYLDLSSPG 319  
DB 282 ISLPESLKRIPIEDGSGEVLSRKVLDDGVONPRAEDLVGKSLVSA-----328  
QY 320 PVEILTVTSVGTISRNVSNTVFFKOHDIIEFFDYTTVLKPSLNTATVKVTRADGN- 378  
DB 329 -----TVILHSGDMQVABESGPIVTPYQIHFTKTPKYFKPMFPLWVFNPDGSP 383  
QY 379 --OLTBERRNNVITVTONYTEYSGNSGQKMEAVQKINYTPVQSGTKIEFPPILE 436  
DB 384 AYRVPVAVQGEDIVQSITQDGVAKLSINTHPQK-----PLSITVTKQELS 432  
QY 437 DSELOLKAFLGSKSMVAHSLFKBPSKTYIQKT-----ADENIKVSGPELVVSGN 490  
DB 433 EAEQ-----ATRTQALPYSTVGNNSNLYLSVLRLTELPEGTINYNFLLRMDRAHE 484  
QY 491 KRKELSYMVVSRGOLVAVGK-----ONSTMFLTPENSWTPKACVIVVY-----IEDDG 540  
DB 485 AKIRYTYILNKKRLLKAGQVREPQDLVVLPLSITTDIFSPRLVAYTYTLIGASGOR 544  
QY 541 EIIISDVLIKIPVQ-----LVFKNKIKLYWSKVAB-----PSEKVSIRISVTPQDSIVGI 589  
DB 545 EVVADSVWVDKSCVSGSLVVKSG-----QSEDRQPVPGQOMTLKIEGDHGAERV-L 595  
QY 590 VAYDKSVNLNANASNDITMENVVHELELYNTGYLGMFMSFAVPOCGELWLTDA-----644  
DB 596 VAVDKGVFLNKKRLLKQSKIWDVVEKADIGCTPGSGKDYAGVPSDAGLTFSSSQQFA 655  
QY 645 -----NLTKDYIDGVYDN-----AEYAEERFME 666  
DB 656 QRAELQCPQPAARRRRSVQLTEKMDKGVKPKELRKCCEGDGRENPMRPSQORTRFIS 715  
QY 667 ENE-----CHIVDIH-----DFSLGSSPHV--RKHPETWIIW-- 696  
DB 716 LGAECKKVFLDCCNYITELRRQHARASHGLARSLNLDIEDIAEENIVSRSEFPESLWNV 775  
QY 697 -----LDTNMGVRIQEPFVTPDPSITGVAFCFVISEDGLGLTITTTVEVLAQAF 746  
DB 776 EDLKEPPNGISTKL-----KNIFLKDSITTWELLAVMSDKKI-CVADPFVTVMQ 827  
QY 747 PFFFLNLPVSVIRGEFALEITIFNVLKDATEVKVJIE--KSKDFDILMTSEINATGH 804  
DB 828 DFFIDLRLPYSVRNEQVEIRAVLYN-RQNKELKVRVELLHNPAFCSLATTKR-----RH 882  
QY 805 QOITLVPSDEGATVLPFIRP--THLGEPIVITVLSPTASDAYTQMLVKAEGIEKSYSQ 862  
DB 883 QOITIPKSLSPVYIVPLKTLQBEVKAAYHHFISDGVKSLKVPPEGIRVKNKV 942  
QY 863 SILDLTDNRL--QSTLTKLTSFSPPPNTV-----TGSE--VQITAGDVILGPSING 910

DB 943 AV-RTDPERLREGVOKE--DIPPADLSQVDPDTESETRILLQGTTPVAQMTEDAVDAE 998  
QY 911 -LASLIRMPYCGGQONMINFAPNIYIILDYLTKKQLTDNLKEK---ALSEFMROGYORELL 966  
DB 999 RLKELIIVTPSGCGQNMIGMTFTVIAYHYLDETEQWEKFGLEKROGGALELIKGYIQOLA 1058  
QY 967 YOREDGFSFAGNYDPSGSTWLSAFVLRCLFLEADPYIDIDQNLVLRHTYTWL-KGHQKSNK 1025  
DB 1059 PRQSSSAFAAFVKEAP--SIWLTAVVVKVFLAVNLIAIDSQVLGAVKWLILEKQKPDG 1116  
QY 1026 EFWDPGRVHSELGGG---NKSPTVITAVITVSLGIRKYQPNIDV-QRSIH-----1073  
DB 1117 VFQEDAPVIHOEMIGGLRNNEKDMALTAFVLISL-----QEAKDICEBOVNSLPGSIT 1170  
QY 1074 ---FLSEFSRSGISDNVTIALITYALSSVSPKAKEALNMLTWRAEQEGMQPFWSSS 1129  
DB 1171 KAGDFLEANY-MNLRSYTVIAIAGYALAOGRKGLPKLNFELT-----TA 1214  
QY 1130 KLSDSWQ---PRSLDIEVAAYALLSHFLQFQTSSEGI-PIMRWLSQRNSLGGPASTQDIT 1185  
DB 1215 KDKNRWEDPGQLYNVEATSYALLA-LLQLKDFDFVFPVVRWLNQORYYGGYGSTQATF 1273  
QY 1186 VALKALSEFAA-LNMTERTNIQVTVTGSPSPPLA-----VVQPMVAVNIS 1229  
DB 1274 MVFOALAQYQKADPHQELNLDVSLQPLPSRSSKITHRIHVESASLLRSEBETKEGFTVT 1333  
QY 1230 ANGFGFATCQLNVVYVNVKASGSSRRRSIQNOEAFDLDVAV-----KENKODLNHVDL 1282  
DB 1334 AEGKGGQGLSVVTVYHAKAKDQLTCNK-----FDLKVTIKPAPETEKEKPODAKNTMIL 1386  
QY 1283 NVCTSFSGPGRSGMALMEVNLISGFMVPE-----AISLSETVKVEY-----DHGKLN 1332  
DB 1387 BICTRYGQDQATMSILDISMTGFPAPDLDKOLANGVDRYISKYELDKAFSDRNTLII 1446  
QY 1333 YLDSVNETQ-FCVNIPIAVRNFKVSNTQDASVSIYDYEPFRQAVRSYNSEV--KLSSCD 1388  
DB 1447 YLDKVSHEDDCLAFKHYQVFNVELIQGAVKVYAYYNLESCITRFVHPEKEDGKLNK-- 1504  
QY 1389 LQSDVQGCPCED 1401  
DB 1505 LCRD-ELCRCAE 1516

RESULT 6  
US-08-487-283A-2  
; Sequence 2, Application US/08487283A  
; Patent No. 6355245  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Mark J.  
; APPLICANT: Matis, Louis A.  
; APPLICANT: Mueller, Eileen Elliott  
; APPLICANT: Nye, Steven H.  
; APPLICANT: Rother, Russell P.  
; APPLICANT: Springhorn, Jeremy P.  
; APPLICANT: Squinto, Stephen P.  
; APPLICANT: Thomas, Thomas C.  
; APPLICANT: Wilkins, James A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT  
; TITLE OF INVENTION: OF INFLAMMATORY DISEASES  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Seth A. Fidel  
; STREET: 25 Science Park (Alexion)  
; CITY: New Haven  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06511  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.4Mb storage  
; COMPUTER: Macintosh Cetrus 610  
; OPERATING SYSTEM: System 7  
; SOFTWARE: WordPerfect 3.0







QY 1233 FGPAICQLNVVNVKASGSSRRRSTQQAFLDVAVKENKDDLNHVD-----LNVT 1286  
Db 1318 DGKATMILTFFYNAQL-----QEKANCNK--FHLNVSE--NIHLNAMGAKMLKICT 1369  
QY 1287 SSGPGRSGMALMEVNLGSEWVPSAIS-----LSETVKVEYDHGKLN-----LYLDS 1336  
Db 1370 RYLGEVDSNTIIDSNLGFLUPDAEDLRKSGVDRIYSRYEVDNNMAQKVAIVIIYNK 1429  
QY 1337 VNETQ--FCVNIPIAVRNFKVNTQDASVSDVYEPYPRQAVRSYNSSEVKLSLSCDCLSDVOG 1395  
Db 1430 VSHSEDECLHFKILKHFEVGFQPGSVKVSYYNLDEKCTKFVHPDKGTGLLNKICIGNV 1489  
QY 1396 CRPECEGASGSH-----HSGVIFPCFKLLYFWE 1425  
Db 1490 CRCAGETCSLHQRIDVPLQIEKACETNVVYKTLRIEE 1533

RESULT 8  
US-09-017-947-2  
; Sequence 2, Application US/09017947  
; Patent No. 6303754  
; GENERAL INFORMATION:  
; APPLICANT: VOGEL, CARL-WILHELM  
; APPLICANT: BREDEHORST, REINHORST  
; APPLICANT: KOCK, MICHAEL  
; APPLICANT: FRITZINGER, DAVID  
; TITLE OF INVENTION: RECOMBINANT PROCVF  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,947  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/662,227  
; FILING DATE: 14-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-0107-0X  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1642 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-017-947-2

Query Match 12.2%; Score 894; DB 4; Length 1642;  
Best Local Similarity 22.5%; Pred. No. 5.5e-65;  
Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56;  
QY 18 AALAV-----APGPRFLVTPAGPIRGGNVTIGVELL-EHCPSQVTVKA-----ELIKTAS 67  
Db 10 AALLIGPPGSHGALYTLITPAVLRTDTEQILVEAHGSDTPKQLDIFVHDPKQKTLF 69

QY 68 NLTVSVLEAGVFKGSEKTLTLPSLPNSADEIYELRVTRGRTQDEILFNSSTLSSETK 127  
Db 70 QTRVDMNAPAGMLVT---PTIEIPEKEVSTDSRONQVYVQVTVGPQVRLEKVLVSYOSS 126  
QY 128 RISFIQTDKALYKPKQEVKPRIVTLFSDFKPYKTSNLILIKPKSNLIQOMLQQSDLG 187  
Db 127 --FLFIQTDKGIYTPGSPVLYRVFSDHNTSKNNKTVIVFQTEGILVS---SNSVDLN 181  
QY 188 VISTFQLSSHPHIGDWSI--OVQNDCTYYQSFQSEYVLPKFEVTLQTP---LYCSMN 242  
Db 182 FF-WPYNLPDLVUSLGTWRIIVAKYHSPENYTAIVDFVAKYVLPSEFVRLQSEKFFYIDGN 240  
QY 243 SKHLNGTITAKYTYGPKVKGDVTLTLPLSPFWGKKNI---TKTEKINGSANFSFNDEE 298  
Db 241 -ENFVSTIARYLYGEEVEG-VAFLVGVKIDDAKSIIPDSLTRIPIDGDGKATLXRD 298  
QY 299 MKNVNDSSNGLSYLDLSSPGFVEILTFTVTSVTGISRNVTNVTFFQKHVDIIIEFFPYTT 358  
Db 299 PRSRFPNLNVLGHTLYAS-----VTVMTEGSDMVVTEQSGIHIIVASPYQIHFTKTPK 352  
QY 359 VLKPSLAFATATKVTADGNQLTLEERRNNVIVTQRNVTYWSGNSGNQKVEAQKI 418  
Db 353 YFKPGMPYELTVYVTPNPDGSPA-----AHVPVSEAF-----HSMGTTLSGDTAKL 398  
QY 419 NYTVPSQSGTFKIEFPFILEDSSELQKAYFLGSKSMVHSLFKSPSKTYIQLKTRDENIK 478  
Db 399 ILNIPLNAQ---SLPITVTRTNHGDLPREROATKSMATAIAYQTGGSGNYLHVAITSTEIK 455  
QY 479 VGS--PFELVVSQN---KRLKELSYMVVSRGQLVAVGK-----QNSTWPSLTPENSWT 526  
Db 456 PGDNLPVNFNVKGNANSLKIKFYTLILNKGIKFKVGRQPRRQGNLVTNHLHITPDLI 515  
QY 527 PKACVIVYVIEDDGEIISDLVKIPVQ-----LVFK--NKILYMSKVKAEPSEKVSURI 578  
Db 516 PSFRFVAYQVGNNEIVADSVVDVKOTCMGTLVVGKDNLIQ-----PGAAMKIL 567  
QY 579 SVTPDSTIVGIVAVDKSVNLMNASNDITMENNVHELELYNTGYLGMPMNSFAVQBQGL 638  
Db 568 E-GDPAARVGLVAVDKAVYVLDNKYKISOAKIWDITIEKDFGTAGSGQNQLGVFEDAGL 626  
QY 639 WVLTDANL-TKD-----649  
Db 627 ALTTSTNLNTKQSAAKCPQANRRRRSSVULLDSNASKAAEFQDQDLRKCCEDVMHENP 686  
QY 650 -----YIDGYD-NAEYAEFRM--BENE-GHIVIDHDF 678  
Db 687 MGYTCEKAKYIQEGDACKAAFLCCRYIKGVRDENQRESELFLARDNEDGFIADSDII 746  
QY 679 SLGSSPHVRKHPPETWIWL-----DTNMGRIYQEFVTPVDSITTSWATGFVISEDLG 732  
Db 747 S-----RSDFPKSWLWLTKDLEEPNSQGISKTSFYLRDSITTTWVLAVSFTPTKG 799  
QY 733 LGLTTTPVELOAFOPFFFLNLPYSVIRGEBFALEITIFNLYKDATEVKVIEKSDKFDI 792  
Db 800 I-CVAEPEIRVMKVFFIDLQMPYSVVKNEQVEIRAILHNVNEDIYVRVELLYNPAF-- 856  
QY 793 LMTSEINATGHQOQTLLVPSEGDATVPIPRPHLG--EIPITVTALSPPTASDVTOMIL 850  
Db 857 --CSASTKGQRYRQOPPIKALSSRAVPFVIVLEQGLHDEIKASVQFALSDGVKRXKL 914  
QY 851 VKAEGIEKSYQSILLDLTDNRLOST-----LKTLSFPPTNTVTGSEVQITAIQDVL 904  
Db 915 VVPEGVQKSIIVTIKALDPRKGVGTQLEVIKAKLDRVDPDTIEFKIILIQGDFVAGII 974  
QY 905 GPSING--LASLIRMPYGCGBQNNMINFAPNI---YILDYLTKKKQLTDNLKELSNFRQ 959  
Db 975 ENSIDGSKNLHLIITPSCGCGEQNMIRMAAPVIATVYLDTTTEQWETLGINRRTAVNQVIT 1034  
QY 960 GYQRELLYQREDDGFSFAGNYDPGSGTWLSAFVLRCP-LEADPYIDIDQNVLHRTYWL- 1017  
Db 1035 GYAQMVKYKADHSHYAAFTN--RASSWLTAYVVKVFAMAAKMWAGISHEIICGGVRWLI 1092  
QY 1018 KGHQKSNCFWDPGRVHSELQG---GNKSPVLTAYIVTISLLGYR-----KYQPNID--V 1068

1093 LNRQPPGAFKFNAPVLSGTMQGGIOGAEBEVLTAFILVALLESKTCNDYVNSLDSSI 1152  
1069 QESIHFLSESPRSISNYLTALITYALSSVGPKEALNMLTWRAEQGGMQFWVSSE 1128  
1153 KKAIVLLKKVEK-LQRPYTTALTAYALA-----AADQLNDRVLMMASTGRDH----- 1201  
1129 SKLSDSWOPSLDIEVAAYALLSHFLQFQSEGPINRWLSRNSRSGGSPASTQDTTVAL 1188  
1202 ---EYNAHTNIEGTSYALLKMKKFDQGTGPIVRWLTQDNFYGETYGTQATVMAF 1257  
1189 KALSEFAALMNTER-TNIQVTVTGSPSPSL-----AVQCP---MAVNTSANG 1232  
1258 QALAEYIOMPTHKDLMDITIELDPREVIRIRYENALLARTVETKLNQDITVTASG 1317  
1233 FGFAICQNVVYVYKASGRRRSRQIBAFDLDAVAKENKODLNHVD-----LNVCT 1286  
1318 DGKATMTILFYNAQL---QEKANVCNK--FHLNVSV--NIHLNMGAKGALMLKICT 1369  
1287 SFGPGRSGHALMEVNLSCGMPSPSEALS-----LSETVKKVEYDHGKLN-----LYLDS 1336  
1370 RYLGEVDSTMTIIDISMLTGFLPDAEDLTRLSKGVDRIYISRYEVDNNMAQKVAIIYLNK 1429  
1337 VNETQ-FCVNIAPVRNFKVNTQDASVIVDYEPERRQAVRSYNSEKLSLSCDCLSDVQ 1395  
1430 VSHSEDECLHFKILKHEVGFQPGSVKVVSYNLDKCTKFYHPDKGTGLLNKICIGNV 1489  
1396 CRPCEDGASGSH-----HSSVIFFCFKLLYFME 1425  
1490 CRAGETCSLNHQERIDVPLQHEKACETNVVDYVYTKLRREE 1533

## RESULT 9

US-09-925-442-2  
Sequence 2, Application US/09925442  
Patent No. 6607897  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
BREDEHORST, REINHORST  
KOCK, MICHAEL  
FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCVF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/925,442  
FILING DATE: 10-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/017,947  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1642 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-925-442-2  
Query Match 12.2%; Score 894; DB 4; Length 1642;  
Best Local Similarity 22.5%; Pred. No. 5.5e-65;  
Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56;  
QY 18 AALAV-----APGPRFLVATGIIRPGNGVITIGVELL-EHCPQSVTVKA-----ELLKTAS 67  
Db 10 AALLIGFPGSHGALYTLITPAVLRTDTEBQILVEAGDSTPKQLDIFVHDFPRKQKTLF 69  
QY 68 NLTVSLAEAGVFEKSGFKTLTLPSLPNSADEIYELRVGTQDBELFNSNLSLSETEK 127  
Db 70 QTRVDMNPAGMLVT---PTIEIPAKEVSTDSRQNYVVQVQVTPQVRLEKVKVLLSYQSS 126  
QY 128 RISVFIQTDKALYKPKQEVKERIVTLSDPKPKYKTSNLLIKDKPSNLIQWLSQSQDLG 187  
Db 127 --FLFIQTDKGIYTPGSPVLRVFSMDHNTSMMKTVIVFETQEGILVS---SNSVDLN 181  
QY 188 VISKTFQLSSHPILGDMSI--QVQVNDQTYQSFVSEYVLPKFEVTLQTP---LYCSMN 242  
Db 182 PF-MPYNLPDLVSLGTWRIVAKYSEHPENYATYFDVAKYVLPSEVRLQSEKFFYIDGN 240  
QY 243 SKHLNGTITAKYTVKPKGVGDTLTLPLSPWGKKMI---TKTFKINGSANFSFNDEE 298  
Db 241 -ENFHSITASYLYGEEVEG-VAFVLPFGVKTDDAKSIPLSLTRIPIIDGDKATLKRD 298  
QY 299 MKNVMDSSNGLSEYLDLSSPGPVEILTITVTSVTGIGSRNVSTNVFPKHQDYIIEFFDYTT 358  
Db 299 FRSRFPNLNELVGHLYAS-----VTVMIESGDMVVVTQSGHIHVASVQIHFTKPK 352  
QY 359 VLKPSLNFTATVKVTRADGNQTLLERRNNVITVTOYNTYVWGSNGSNQKMEAVQKI 418  
Db 353 YFKGMPYVELTVVYVTPDSPA-----AHVSVWSEAF-----HSMGTLLSDGTAFL 398  
QY 419 NYTVPSQGTFFKIEPILLESSELOKAYFLGSKSMVAHSLFKSPSKTYIQLKTRDENIK 478  
Db 399 ILNIPLNAQ---SLPITVTRNHGDLPRERQATKNTAIAYQTQGGSGNYLHVAITSTEIK 455  
QY 479 VGS--PFELVYSGN---KELKELSVWVSRGQVAVGK-----QNSTMFLSTPENSWT 526  
Db 456 PGDNLVFNPNVKNANSKQIKYFTYLLNKGIKFKVGRQPRRDGQNLVTMLNHLITPDLI 515  
QY 527 PKACVIVYVIEDDGEIISDLKIPVQ-----LVFK--NKIKLYSVKVAEPSEKVSURI 578  
Db 516 PSFRFVAYYQVGNNEIVADSVMVDVKDTCMTGLVVGKGNLIQM-----PGAMKIKL 567  
QY 579 SVTQPDSTVIGVAVDKSVNLMNASNDITMENVVHELELYNTGYLGMFMNSFAVQFCGL 638  
Db 568 E-GPEGARVGLVAVDKAVYVLDKVKISQAKIWDTEKSDFGCTAGSGQNNIGVFEDAGL 626  
QY 639 WVLTDANL-TKD----- 643  
Db 627 ALTTSTNLTKQSAKCPQANRRRSSVLLLDNSAKAAEFQDQDLRKCCEVWHENP 686  
QY 650 ---YIDGYVD-NAEYAEFRM--BENE-GHIVDTHDF 678  
Db 687 MGYTCEKEAKYIQSDACKAAFLCCRYIKGVRENQRESELFLARDNEDGFIADSDII 746  
QY 679 SLGSSPHVRKHPETIWL-----DTNMGVRIYQVEFVTVPSDITSWATGVVISDLG 732  
Db 747 S-----RSDFPKSLMLTKDLTEEPNSQGISKTSFYLRDSITTVVVLAVSFTPTK 799  
QY 733 LGLTTTPVELQAFQPFIFLNLPSYVIRGEEFALEITFYNLKDATBEVKVIEKSDFDI 792  
Db 800 I-CVAEPYEHKMWFFIDLQMPYSVVKNEQVEIRAILHNYVNEIDIVRVVELLYNPAF-- 856  
QY 793 LMTSSEINATGHQOITLLVPSEDGATVLPFIRPHLG--EIPITVTALSPASDAVTQMIL 850

Db 857 --CSASTKGORYQOPPIKALSRVFPVIVPLEQGLHVDVEIKASVQEAUMSGVRKKLK 914  
Qy 851 VKAEGIEKXSQSILDLTDNRLOST-----LKTLSFSPPTNTVTSRVRQITAGDVL 904  
Db 915 VVPEGVQKSVITVKLDPRAKGVGGTQLEVIKARKLDRVPDTEIETKIIIQDPAQII 974  
Qy 905 GPSING--LASLRMPYGCCEQWNPAPNI---YILDYLTKKQLTDNLKEALSPMQ 959  
Db 975 ENSIDGSKLHLIITPSGCGEQMIRVAAPVIATYLDTTQOWETLGINRRTEAVNQIYT 1034  
Qy 960 GYORELLYQREDGFSFAGFNDVPSGWTLSAFVLRCP--LEADPYIDIDQNLVLRHTWTWL- 1017  
Db 1035 GYACQWYKKADHSYAFTN--RASSWLTAYVUVKVPAMAAMVAGISHIICGVWRLLI 1092  
Qy 1018 KHQKSNGETPDRGVHSELQ--GNKSPVLTAYIVTSLGYR-----KYQPNID--V 1068  
Db 1093 LNRQOPDGAFAENAPVLSGTWQGIQGAEEVYLTAFILVALLESKTIENDYVNSLDSSI 1152  
Qy 1069 QESTHPLESEFSRISGIDNYTLALITVALSVSGPKAEALNMLTWRAEQEGGQFVVSSE 1128  
Db 1153 KKATNYLLKKYK-LQRPYTTALTAYALA-----AADQLNDRVLMASSTGRDHV- 1201  
Qy 1129 SKLSDSQPRSLDIEVAAYALLSHFLQFOTSEGIPIMRWLSRQNSLGGFASQTDTTVAL 1188  
Db 1202 ---EYNAHTHNIEGTSYALLALLKKMKFDQTPVIRWLTQNFYGETYQTOATWAF 1257  
Qy 1189 KALSEPALMNTER-TNIQVTVGPSPSP------AVQPP---MAVNISANG 1232  
Db 1258 QALAEYBIQETHKDLNLDITIELPREVIRYINYNENALLARTVETKLNQDITVTASG 1317  
Qy 1233 FGFAICOLNVVYVVKASGSSRRRSIQNEAFDLDAVAKENKDDLNHVD-----LNVCT 1286  
Db 1318 DGRATWILFYNAQL-----QERANVCN--FHLNVSVE--NIHLNAGAKGALMKICT 1369  
Qy 1287 SFGSGRSGMALMEVNLISGFMVPSAIS-----LSETVKVBYDHGKLN-----LYLDS 1336  
Db 1370 RYLGEVDSTWITIDISMLTGLPDAEDLTRLSKGVDRYISRYEVDNMMQAKVAVIYLNK 1429  
Qy 1337 VNETO-PCVNIAPVRNFKVSNTOVASIVDYVPEPRQAVRSYNSEVKLSCDLCSDVQG 1395  
Db 1430 VSHSEDLHFKLKHGEVGFQPGSVKVSYSYNLDEKTKFVHPDKGTGLNKKICIGNV 1489  
Qy 1396 CRPCEDGASGSH-----HSSVIFFCFKLLYFME 1425  
Db 1490 CRCAGETCSLNHOERIDVPLQIEKACETNVVYVYKTLRIEB 1533

## RESULT 10

US-08-447-411-45  
; Sequence 45, Application US/08447411  
; Patent No. 5773243  
; GENERAL INFORMATION:  
; APPLICANT: FRITZINGER, DAVID C.  
; APPLICANT: BREDEHORST, REINHARD  
; APPLICANT: VOGEL, CARL-WILHELM  
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,411  
; FILING DATE:

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/043,747  
; FILING DATE: 07-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Obion, No. 5773243man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-101-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1642 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-447-411-45

Query Match 12.0%; Score 885; DB 1; Length 1642;

Best Local Similarity 22.4%; Pred. No. 3.1e-64;

Matches 359; Conservative 296; Mismatches 63; Indels 276; Gaps 56;

Qy 18 AALAV-----APGPRFLVTAQIIRPGNVTIGVELL-EHCPSSQVTVKA---ELLKTAS 67  
Db 10 AALLGFGSSHGALYTLITPAVLRTDEEQLLVEAHGDSSTPKQLDIFVHDFPRKQKTLF 69  
Qy 68 NUTSVLBAEYFEGKSPKTLTLPSPNSADEIYELVGTQDEILFNSSTRLSFETK 127  
Db 70 QTRVDMNPAAGMLVT---PTIEIPAKVSTDSRQNYVYVQVTPQVRLKVVLLSYOSS 126  
Qy 128 RISVFIQTDKALYKPKQEVKFERIVTLFSDFKPYKSLMILIKDPKSNLIQQWLSQOSDLG 187  
Db 127 --FLTIQIDKGIYTPGSPVLIRVFSMDHNTSKXNKIVIVEFTQPEGILVS---SNSVDLN 181  
Qy 188 VISKTFLQSSHPILGDWSI--QVQVNDQTYYSQVSEYVLPKFVTLQTP---LYCSMN 242  
Db 182 PF-WPYNLPDLVSLGCTWRIVAKYHSPENYATFVPRVYVLPSPFVRLOPQSEKFFYIDGN 240  
Qy 243 SKHLNGTTTAKTYTKPKVKGVDLTFLPLSPWGKKNI-----TKTFKINGSANFNDDEE 298  
Db 241 --ENFHVSIATRYLYGEEVEG-VAFVLFVGKIDDAKKSIPDSLTRIPIDGGKATKTKDT 298  
Qy 299 MKNVMDSSNGLSEYLDLSSPGVEILTTVTSVTSISRNVSTNVFPFKQHDVILIEFFDYTT 358  
Db 299 FRSRFPNLNVLGHLYAS-----VTMTSGSDMVVTEQSGIHIVASPYQIHETKTPK 352  
Qy 359 VLKPSLNTATVKTTRADGNQLTLEERNNVVITVQRNYTEYWSGNSGKQMAVOKI 418  
Db 353 YFKPGMPYELTVYVTPNPDGSPA-----AHVPVYSEAF-----HSMGTTLSDGTAKL 398  
Qy 419 NYTVPSQSGTFKIEFFILEDSSSELQKAYFLGSKSMVAHSLFKSPSKTYIOLKTDENIK 478  
Db 399 ILNIPLNAQ---SLPITVTRTHGDLPRERQATKSWTAYQTQGGSGNYLHVATSTIK 455  
Qy 479 VGS--PFELVWSGN---KRLKELSYMVVSRQLVAVGK-----QNSTMTSLTPENSMT 526  
Db 456 PGDNLVVKFQCQGCQNSLKQIKYFYILNKGKIFKVGQRPRRDQGNLVNMLHTPDLI 515  
Qy 527 PKACVIVVYIEDDGEIISDVLKIPVQ-----LVFK--NKILYWSKYKAPSEKVSURI 578  
Db 516 PSFRFVAYVQGNNEIVADSVWVDVKDTCMGTGLVYKGDNLIQM-----PGAAMKIKL 567  
Qy 579 SVTQPDSTVIGIVADKSVNLMNASNDITWENVVHELELYNTGYILGMFMNSPAVFEQGL 638  
Db 568 E-GDPCARVGLVADVAVYVNDKYKISOAKIWDIETKSDFGCTAGTAGGNLGVFEDAGL 626  
Qy 639 WVLTDANL-TKD-----  
Db 627 ALTTSTNLNLTORSAAKCPQFANRRRRSSVLLSDNSAKAAEFQDQDLKCCEDVMHNENP 686  
Qy 650 -----YIDGYVD-NAEVAERFM--EENE-GHIVDIHDF 678

Db	687	MGYTCEKRAKYIOEGDACKAAFLCECCYIKGVARDENQRESELFLARDNDEGFIADSDII	746
Qy	679	SLAGSSPHVRKHFPETWTWL-----DTNMGYRIYQBEFVTPDPSITSWATGFIISDLG	732
Db	747	S-----RSDFPKSWLWFKDLTEEPNSQGISSKTMSFYLRDSIITWVLVASFTEPKG	799
Qy	733	LGUTTPVELQAOQPPFIINLPSYVIRGBEPALEITIIFYLKDATBEVKVIEKSDKFDI	792
Db	800	I-CVAEYEIRVMKVFFIDLOMPYSVYVKNQVFEIRAILHNYVNEDIYVRVELLYNPAF--	856
Qy	793	LMTSSSEINAGHOQTLLVPSEGDATVLPFIRPHTLG--EIPITVTALSPASDAVTCMIL	850
Db	857	--CSATKGORYQOPPIKALSRAVPFVIVPLEQGLHDVEIKASVQEALWSDGVKKLK	914
Qy	851	VKAEGTEKYSQSILLDLTNRIQST-----LKTLSFSPPNVTGTSERVOITAGDVL	904
Db	915	VWPEGVOKSVTIVKLPDRAKGVGGTQLEVIKARKLDRVPDTEIETKIIIOGDPVAQII	974
Qy	905	GPSING--LASLIRMPYGCCEQNNINPAFNI---YILDYLTKKQLTDNLKEKALSPMRQ	959
Db	975	ENSIDGSKLNLHIITPSCGCEQNWIRMAAPVIATYYLDTTEQWETLGINRTEAVNQIVT	1034
Qy	960	GYORELLOYREDSGFSAGFYDPSGTSWLGAFLVURCF-LEADPYIDIDQNVLHRTYTWL-	1017
Db	1035	GYAQOMYKKAHDSYAAFTN--RASSSWLTAYVYKVPAMAAMKAVAGISHIEIIICGVRWLI	1092
Qy	1018	KGHQKNGEFPWDCGRVTHSELQG--GNKSPVTLTAVIVTSLLYGR---KYQPNID--V	1068
Db	1093	LNQOPDCAKFNAPVUSGTMQGGIOGAEBEYVLTAFILVALLSKTICNDYNSLDSII	1152
Qy	1069	QESIHFLESEFSGISDNYTALITYALSSVGSGPKAKEALNMLTWRAEQEGGMOFWVSSE	1128
Db	1153	KKATNYLLKYEK-LORPYTALTAYALA-----AADQLNDRDLVMAASTGSDHM----	1201
Qy	1129	SKLSDSQPRLDTEVAAYALLSHFLQFOTSEGIPIMRWLSRONSILGGFASQDITVAL	1188
Db	1202	-----EENYANTHNIEGTSYALLALLKMKKFDQGPVIRWLTQDNFYGETYGOQTAWAF	1257
Qy	1189	KALSEFAALMNTER-TNIQVTVTGPSPSPU-----AVQOP-----MAVNISANG	1232
Db	1258	QALAEYBIQPTHKDLMLDITIELPDREVPYRINYENALLARTVETKLINQDITFASG	1317
Qy	1233	FGFAICOLNVVYNVKASGSSRRRSIQOEAFLDVAKENKDDLNHVD-----LNVCT	1286
Db	1318	DGKATMTILFYNAQL-----QEKANVCNK--FHLNVSE--NIHLNMGAKGALMKICT	1369
Qy	1287	SFSGPGRSGMALMEVNLISLGFMPVSPSEALS-----LSTVTKVEYDGHKLN-----LYLDS	1336
Db	1370	RYLGEVDSWTWIIDISMLTGFLPDAEDLTSLSGVDYIRSYREVNDNMAOKVAVIYLNK	1429
Qy	1337	VNETQ-PCVNI PAVRNFKVNTODASVSIYDVYEPREQAQRSYNSSEVKLSSCDLCSDVQG	1395
Db	1430	VSHSEDECLFKILKHFEVGFIOGYSVKVYSYVNLDEKCTKTFHPDKGTGLMKICIGNV	1489
Qy	1396	CRPCEDGASGSH-----HSSVIFIFCFLLYFME	1425
Db	1490	CRGAGETCSLNIHOERIDVLOIEKACETWNVDVYVTKKLRISEE	1533

## RESULT 11

RESULTS II  
US-08-662-227-35

US-08-082-227-33  
: Sequence 35. Application US/08662227

: sequence 33, APPLIC  
: Patent No. 5922320; FACILE NO. 3922320  
: GENERAL INFORMATION:

GENERAL INFORMATION: CARL-WILHELM  
APPLICANT: VOGEL:

APPLICANT: BREDEHORST, REINHORST

APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL

APPLICANT: ROCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID

APPLICANT: FRIZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCVF

FILE OF INVENTION:	REC
NUMBER OF SEQUENCES:	39

; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS: MCCI, EILAND MATER & NEUSTADT.  
; ADDRESSEE: ORION SPIYAK

ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/662,227  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1136-0107-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1648 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-662-227-35

Query Match	12.0%;	Score 880;	DB 2;	Length 1648;			
Best Local Similarity	22.7%;	Pred. No. 8.2e-64;					
Matches	365;	Conservative 295;	Mismatches 664;	Indels 284; Gaps 59;			
Qy	18	AALAV-----AGPRLVTA	GIIRPGNV	TIGVELL-EHCP	SQVTKA-----ELIK	TAS 67	
Db							
Qy	10	AALLIGFPSS	HGALYTLITPAV	RTDTEQILVEAH	GDSTPKQLDIFV	HDPRKQTLF 69	
Db							
Qy	68	NUTSVLEAG	VFKEGSKFTLTP	LSPLNLSADIE	YELRVGTQD	BEILFSNSTRLSFETK 127	
Db							
Qy	70	QTRVDMNP	PAGGLAVT---PT	BIPAKEVSTDR	QNOQVYVVVQ	TGPGVRLKXVLLSYQSS 126	
Db							
Qy	128	RISVRIQT	KALYKPKQEK	YKFRIVTLFS	FKPKYTSNLTL--	KDPKSNLIQWLSQQSD 185	
Db							
Qy	127	--FLFIQT	DKGIYTPGSP	VLVRFVSM--	DHHTSKMKTV	IVFQTEGILVS---SNSVD 179	
Db							
Qy	186	LGVISKTF	OLSHPI	LGDSKI--Q	VNDQTYQSFQ	VSEYVLPKPEVTLQTP---LYCS 240	
Db							
Qy	180	LNPF--WP	YNLPDLVLS	GTWRIVAK	YEHSPENTAY	FDRVKYVLPSEVRLQPSKEFFYID 238	
Db							
Qy	241	MNSKHLNG	ITAKYTYGK	QVKGDVTLT	FLPLSPWGKKNI---	TKTFKINGSANFEND 296	
Db							
Qy	239	GN--ENPH	VSITARYLYG	EEVEG--VA	PLFGKIDDAK	KSIPLSLRIPIDIGDCKATLKR 296	
Db							
Qy	297	EEMKNVMS	DSNGSLSE	YDLSSPGP	VEILTVTESVT	GISGRNVTNNVFFKHQDYIIIEFFDY 356	
Db							
Qy	297	DTFRSFP	NLNLVGH	TLYAS-----	VTVMTESSG	DMVVTQESGIHIVASPYQHFTKT 350	
Db							
Qy	357	TTVLKPSL	NFTATVKT	RADGNQLT	LIEERNNV	IVITQBNYTEYWSGNSGNQKMEAVQ 416	
Db							
Qy	351	PKYFKG	PMYEULTV	VYVNTNPD	GPSA-----	AHVPVVEAF-----HSMGTTLS	DGTA 396
Db							
Qy	417	KINYTV	PQSGTEK	IEPPILED	SSLOKAYFG	LSKSSMAVHSLFKSPKTYIQLKTRDEN 476	
Db							
Qy	397	KLILNPL	NAQ--SLPI	TVRTHGDL	PRERQATK	SMTAIAVQTQGGSNYLHVATISTE 453	
Db							
Qy	477	IKVGS--	PRELVSGN	----KBL	KELSYMVV	SRGQLVAVGKQNS-----TW-PSLTPE 522	
Db							
Qy	454	IKPGDNL	PVNFNVK	GNANSLKQI	KYFTYIL	ILNKGKIFKVRPRDRGQNLVTNLHITPD 513	
Db							
Qy	523	NSMTKR	ACVIVYIE	DDGIIISD	VLKIPVQ-----	LVPK--NKILYWSKVKAEPSEKV 574	
Db							

Db 514 LIPSPR--FVAYQVGNNEIVADSVVWVKDKTCWGLTVKGDNLQMPGAAMKIKLEGDF 571  
QY 575 SLRISVTPQPSIYIGIVAVDKSVNLMASNDITWENVVHELELYNTGYLGMFMNSFAVFO 634  
Db 572 GAR-----VGLVAVDKAVTVLNDKYKISAKIWDITKSDFCCTAGSGONNLGVE 622  
QY 635 ECGLVLTDLNL-TKD----- 649  
Db 623 DAGLALTTSTNLNTKQSAKCPQANRRSSVLLLDNSNASKAABFQODLRKCCEDVM 682  
QY 650 -----YIDGVYD-NAEVAERFM--EENE-CHIVD 674  
Db 683 HENPMGYTCRKRAKYIQEGDACKAFLCCRYTKGVDRDENQRESEFLARDNEDGFAD 742  
QY 675 IHDFSLGSSPHVKHPETWML-----DTNMGYRIYQEFFVTPDSTISWATGVFIS 728  
Db 743 SDIIS-----RSDFPKWLMLTKDLTEEPNSQGISSKMTSFLRDSITWVLAVSFT 795  
QY 729 EDGLGLTTPVBLQAFQFFIFNLIPYSVIRGEBFALFITPNYKQATEVKVIEKSD 788  
Db 796 PTKGI-CVABPYBIRYMKVFFIDLOMPYSYVKNQOEIRAILHNYVNEIDYVRVELLYNP 854  
QY 789 KFOILMTSSINATGHQOOLLVPSDGTATVPFIRPTHLG--EIPITVATLSPTASDAYT 846  
Db 855 AP-----CSASTKQCRVQRPPIKALSRAPFVIVPLEQGLHDEVEIKASVQEAALNSDGV 910  
QY 847 QMILVKAEGIEKSYOSIILLDTNRLQST-----LKTLSFSPPTNTVTGSEVQITAI 900  
Db 911 KKLKVVPEGVOKSIVITVKLDPRKGVGGTQLEVIKARKLDORVPDTEETETKIIIGDPV 970  
QY 901 GDVLGPSING--LASITRMPYGGEGONMINFANI---YILDYLTKKQLTDNLKEKALS 955  
Db 971 AQIENSIDGSKNLHLIITPSGCGEONMIRMAAPVIATYLDTEQWETLGINRRTAEN 1030  
QY 956 FMRQGYORELLYQREDSFSAFNGPSGSTWLSAFVLRCP-LEADPYIIDQNVLHRTY 1014  
Db 1031 QIVTGAQVYKADHSAFAFN--RASSMLTAYVVKVFAAKWAGISHEIICGV 1088  
QY 1015 TWL-KHQKSNGEFDPGRVHSELQ---GNKSPVTLTAYIVTSLGYR----KYQPM 1066  
Db 1089 RWILNRPQPDGAFKFNAPVLSGTMOGGIQAEEVYLTAFILVALLESKTCINDYVNSL 1148  
QY 1067 D--VQBSIHFLSEFSGISDNVTALITVALSSVGSPPAKALNMLTWRAEQEGMQWF 1124  
Db 1149 DSSIKKATNYLLKKYEK-LQRPYTTALTAYALA-----AAQNLNDRVLMMASTGRDH 1201  
QY 1125 VSSEKLSDSQWPRSLDIEVAAVALLSHFLQFQTSBGIPIMRWLSQRNSLGGFASTQPT 1184  
Db 1202 -----BEYNARHTNIEGTSVALLALLKMKKFDQTPVIRWLTDQNFYGETYGTQAT 1253  
QY 1185 TVALKALSEFAALMNTER-TNIOVTVTGSPSPPL-----AVVQP---MAYNI 1228  
Db 1254 VAFQALAEYIOMPHKQNLNLDITIELDPREVPIRYRYNENALLARTVETKLNQDITV 1313  
QY 1229 SANGFGFAICQLNVNWKVNSKASGSSRRRSRSTQNOEAFDLQVAVKENKDDLNHVD-----L 1282  
Db 1314 TASGDGKATMTILTFYNAQL---QEKANVCNK--FHLNVSVB--NIHLNANGAKGALM 1365  
QY 1283 NVCTSFSGRSGSMALMEVNLISGFMVPSAIS-----LSETVKVVEYDHGKLN-----L 1332  
Db 1366 KICTRYLGEVDSTMTIIDISMLTGLFADIEDLRLSKGVDRVYSRYEVDNNMAQKVAVII 1425  
QY 1333 YLDSVNETQ-FCVNIPAVRNFKYSNTQDASVSVVDVYEPERRQAVRSYNSEVKLSSCDLCS 1391  
Db 1426 YLNKVSSEDECLHPKILKHFEVGFQPGSVKVSYSYNNLDEKCTKYHFKDGTGLLNKIC 1485  
QY 1392 DVQGCRCPCDAGSGSH-----HSSVIFIFCFKLLYPME 1425  
Db 1486 IGNVCRAGETCSLSNEQERIDVPLQIERACETNVDYVYKTKLLREE 1533

RESULT 12

US-09-017-947-35

; Sequence 35, Application US/09017947  
; Patent No. 6303754  
; GENERAL INFORMATION:  
; APPLICANT: VOGEL, CARL-WILHELM  
; APPLICANT: BREDEHORST, REINHORST  
; APPLICANT: KOCK, MICHAEL  
; APPLICANT: FRITZINGER, DAVID  
; TITLE OF INVENTION: RECOMBINANT PROCVF  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,947  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/662,227  
; FILING DATE: 14-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORVAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-0107-0X  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1648 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-017-947-35

Query Match 12.0%; Score 880; DB 4; Length 1648;  
Best Local Similarity 22.7%; Pred. No. 8.2e-64;  
Matches 365; Conservative 295; Mismatches 664; Indels 284; Gaps 59;

QY 18 AALAV-----APGRFLVTPAGIIRPGNVITIGVELL-EHCPSQVTVKA----ELLKTAS 67  
Db 10 AALLIGPGSSHGALYTLITPAVIRDTTEEQILVEAHGDSPTKQLDIFVHDFPRKQKTLF 69  
QY 68 NLTVSVLEAEGVFKSGFKTLTLPFLPNSADEIYELRVTRTQDEILFNSNTRLSPTK 127  
Db 70 QTRVDMNPAGMLVT---PTIEIPAKEVSTDSRQNVQVQVTVGPQVRLEKWLVSQSS 126  
QY 128 RISVFIQDKALYKPKQEKVRIVTLPSDFPKYKTSNLILI--KDBKSNLIQWLSSQSD 185  
Db 127 --FLFIQDKGIYFGSPVLYRVFSM--DHHTSKNKTIVIVEFQTPGILVS---SNSVD 179  
QY 186 LGVISKTPQLSSHPILGDWSI--QVQNDQTYQSFQVSEYVLPKFEVTLQTP---LYCS 240  
Db 180 LNFF-WPYNLPDLVSLGTWR-IVAKYHSPENYATFVDRKIVLPSEFVRLQSEKFFYID 238  
QY 241 MNSKHLNNTITAKTYGKPVKGVDTLTLPLSPFGKKNI-----TKTFKINGSANFSND 296  
Db 239 GN-ENFHVISITARYLYGEEVEG-VAFVLFGVKIDAKKSIDPSLTRIPIDGDGKATLKR 296  
QY 297 EEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGSRNVSTNVPFKQDYIIIEFFDY 356  
Db 297 DTFRSRFPNINELVGHILYAS-----VTVMTEGSDMVVTEQSGIHIVASPYQIHETKT 350

QY 357 TTVLKPSLNFATVKTTRADGNQITLERNVTVITQRTNYTEYSGNSGNQKMEAVQ 416  
Db 351 PKYFKPMKVELTVYVNPDSFA-----AHVPVSEAF-----HSMGTLSDGTA 396  
QY 417 KINYVTPQSSTKIEFFILBDSSELOKAYFLGSKSSMAVHSFKSPSKTYIQLKTRDEN 476  
Db 397 KLILNIPLNAQ---SLPITVTRNHGDLPREROATKSMATAIAYQTGGSGNLYHVAITSTE 453  
QY 477 IKVGS---PFELVSGN---KRLKELSYMVVSGQLVAVGKONS-----TM-FSLTPE 522  
Db 454 IKPGDNLVFNFNKGNANSLOKIKYFTYILNKGKIPKVGQRPRRQONLVTNNLHITPD 513  
QY 523 NSWTPKACVIVYIEDDGEIISVLKIPVQ-----LVFK--NKIKLYMSKVKAEPSEKV 574  
Db 514 LIPSFR--FVAYVQVGNNEIVADVVDVKDTCWGLVVKGDNLIQMPGAAMKILEGDF 571  
QY 575 SLRISVTPDSIVGIVAVDKSVNLMNASNDITWENVVHELELYNTGYLGMPFNSTFAVQ 634  
Db 572 GAR-----VGLVAVDRAVTVLNDKYKISQAKIWDTIKSDFGCTAGSGQNNLGVEF 622  
QY 635 ECGIWLTLTDLNLT-KD-----649  
Db 623 DAGLALTSTNLNTKQSAKCFOPANRRRRSVLLDSNASKAAEFQDQDLKXCCEDVM 682  
QY 650 -----YIDGVYD-NAEYAEFRM--EENE-GHIVD 674  
Db 683 HENPMGYTCBRAKYIOEGDACKAAFLCCRYIKGVREDCNRESEFLFLARDNEDGFAD 742  
QY 675 IHDFSLGSSPHVRKHPETWIL-----DTNMGYRIYQEFVTVPDSITSWATGFVIS 728  
Db 743 SDIIS-----RSDFPKWLTLTKOLTPEPNSQGISSTMSFYLRDSITTVVLAVSET 795  
QY 729 EDGLGLTLTPVELQAPQFFILNPLSVIRGEEPALEITFIENLYLKDATEVKVIEKSD 788  
Db 796 PTXGI-CVAEPYELRVKVFIDLOPYSVVVKNQOEIVRAILHNYNEDYVRVELLYNP 854  
QY 789 KFDILMTSSINATHQOTLLVSEDAVTLPIRPHLG--BIPITVLTALSPASDAVT 846  
Db 855 AF-----CSASTKGORYQRPPIKALSSRAVPFVIVPLEQGLHDVEIKASVQEAALMSDGYR 910  
QY 847 QMILVKAEGIEKYSQSILDLDTNRLQST-----LKLTSFSPFPNTVTGSEVRQITAI 900  
Db 911 KKLKWPVEGVQKSIVTIVKLDPRAKGVGTQLEVIKARKLDRVPDTEIETKIIIOGDFV 970  
QY 901 GDVLGPGSING--LASLRIMPYGCQEQNMIFAPNI---YILDYLTKKKQOLTONLKEKALS 955  
Db 971 AQIIEISIDGSKNLHLIITPSGCGEQNMIRMAAPVIATVYLDTEQWETLGINRRTEAVN 1030  
QY 956 FMQCGYORELLYQREDSFSAFGYDPSPGSTLSAFVLRFC-LEADPYIDIDQNVLRHY 1014  
Db 1031 QITVGYAQQWYKKAADHSYAFTN--RASSSWLTAYVVRVFAAAKMWAGISHEIICGV 1088  
QY 1015 TWL-KGKQSGEFWDPRVHSELQ--GNKSPVLTAYIVTSLLYR---KYQPN 1066  
Db 1089 RWLILNEQPDGAFKENAPVLSGTMOGGIOGAEEVVLTAFILVALLESKTIENDVNSL 1148  
QY 1067 D--VQESIHLESEFSGISDNTLALITYALSSVGSPPAKEALNMLTWABOEGGQW 1124  
Db 1149 DSIKIKATNLLKKYK-LQRPYTTALTAYALA-----AADQLNDRVLMMAASTGRDH 1201  
QY 1125 VSSEKLSDSWQPSRLDIEVAVALSHFLQFQTSBGPIMRWLSQRNSLGSFASTQDT 1184  
Db 1202 -----EYNATHNIBGTSVALLALLKWKXFDQGTGPIVRLTQNFVGYGTQAT 1253  
QY 1185 TVALKALSEFAALMNTER-TNIOVTVTGSPSSPGL-----AVQP---YAVNI 1228  
Db 1254 VMAFQALAEYEQMPTHKDLNLTITELPDREVPFIRYINENALLIARTVETKLNQDITV 1313  
QY 1229 SANGFGFALCOLNVVYNKASGSSRRRSRSONEAFDLDVAVKENKDLNHDV-----L 1282  
Db 1314 TASDGGATWILTFFYNAQI-----QEKANVCNK--FHLNVSVZ--NHLNMAKALML 1365  
QY 1283 NVCTSPSGPGRSGMALMEVNLSSGFMVPSAIS-----LSETVKVVEYDHGKLN-----L 1332

Db 1366 KICRYLGEVDSTWTIIDISMLTGLFPLDABDLTFLSKGVDRYISRYEVDNMAQKVAVII 1425  
QY 1333 YLDSVNETQ-FCVNI PAVRNFKUNTOQASVISVDYEPBROQVRSYNSVSKSSCDLCS 1391  
Db 1426 YLNVKSHSEDECLPKILKHFEVGIQFSGVKVYSYNNLEKCTKFYHPDKRGTLNKC 1485  
QY 1392 DVQGRPCEDCAGSHH-----HSSVIRIFCFKLLYFME 1425  
Db 1486 IGNVCRAGETCSSLNQERIDVPLQIEKACETNVVYVYTKLLRIEE 1533  
RESULT 13  
US-09-925-442-35  
; Sequence 35, Application US/09925442  
; Patent No. 6607897  
; GENERAL INFORMATION:  
; APPLICANT: VOGEL, CARL-WILHELM  
; BREDEHORST, REINHORST  
; KOCK, MICHAEL  
; FRITZINGER, DAVID  
; TITLE OF INVENTION: RECOMBINANT PROCVF  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/925,442  
; FILING DATE: 10-Aug-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/017,947  
; FILING DATE: <unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-0107-0X  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1648 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
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Query Match 12.0%; Score 880; DB 4; Length 1648;  
Best Local Similarity 22.7%; Pred. No. 8.2e-64;  
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RESULT 15
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; Sequence 34, Application US/08662227
; Patent No. 5922320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-662-227-34

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Best Local Similarity 24.4%; Pred. No. 8.2e-54;
Matches 301; Conservative 208; Mismatches 477; Indels 247; Gaps 46;

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Qy 469 QUKTRDENIKVGS--PFELVVGNN-----KELKELSYWVSRGOLVAVGKNS-----TM 516

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Search completed: August 10, 2004, 19:34:42  
Job time : 34 secs

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3	1690.8	39.4	1880	13	US-10-112-944-160	Sequence 160, App	
4	1017	22.7	1448	16	US-10-364-237-1040	Sequence 1040, App	
5	975.4	22.8	1459	13	US-10-876-774-601	Sequence 601, App	
6	730.8	17.0	1300	15	US-10-133-013-223	Sequence 223, App	
7	541.6	12.6	875	15	US-09-820-649-48	Sequence 48, Appl	
8	541.6	12.6	875	15	US-10-160-162-48	Sequence 48, Appl	
9	525	12.2	821	13	US-10-111-462-208	Sequence 208, App	
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306 CTCACGAAGATATATATGATGTGTTTATGACATGCGAGATATGCTCAGAGGTTTATG 365  
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QY	4165	CTTTGAGTGAATGTCAGGCTGCGTCTCTGTGAGGATGGAGCTTCAGGCTCCCATCAT	4224
Db	2586	CTTTGAGTGAATGTCAGGCTGCGTCTCTGTGAGGATGGAGCTTCAGGCTCCCATCAT	2645
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US-10-108-260A-953			
; Sequence 953, Application US/10108260A			
; Publication No. US20040005560A1			
; GENERAL INFORMATION:			
; APPLICANT: HELIX RESEARCH INSTITUTE			
; TITLE OF INVENTION: No. US20040005560A1e1 full length cdna			
; FILE REFERENCE: HI-A0106			
; CURRENT APPLICATION NUMBER: US/10/108, 260A			
; CURRENT FILING DATE: 2002-03-27			
; NUMBER OF SEQ ID NOS: 5458			
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; SEQ ID NO 953			
; LENGTH: 2273			
; TYPE: DNA			
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Db	246	GAGTGTCTCAAGACAGATCAAACTCTGCTGTCTGTCTGCTGGAAGCAGAGAGTCTTT	305
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QY	961	GTAGAAATTTTAAACACAGTGCACAGATCACTTACAGTATTTCAAGAAATGTAGCACT	1020
Db	1026	GTAGAAATTTTAAACACAGTGCACAGATCACTTACAGTATTTCAAGAAATGTAGCACT	1085
QY	1021	AATGTGTTCTTCAAGCAACATGATTTACATCATTTGAGTTTCTTGTATTTACTACTGCTTG	1080
Db	1086	AATGTGTTCTTCAAGCAACATGATTTACATCATTTGAGTTTCTTGTATTTACTACTGCTTG	1145
QY	1081	AAGCCATCTCTCAACTTCAAGCCACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1140
Db	1146	AAGCCATCTCTCAACTTCAAGCCACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1205
QY	1141	ACTCTTGAAGAAAGAAAGAAATAATGTAGTCAATACAGTGCACAGAGAACTATACTGAG	1200
Db	1206	ACTCTTGAAGAAAGAAAGAAATAATGTAGTCAATACAGTGCACAGAGAACTATACTGAG	1265
QY	1201	TACTGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAAGAAATAAATATAT	1260
Db	1266	TACTGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAAGAAATAAATATAT	1325
QY	1261	ACTGTCCCCCAAGCTGGAACCTTTTAAAGTGAATTTCCCAATCTCTGAGGATTCAGTGTG	1320
Db	1326	ACTGTCCCCCAAGCTGGAACCTTTTAAAGTGAATTTCCCAATCTCTGAGGATTCAGTGTG	1385
QY	1321	CTACAGTTTGAAGGCTATTTCTTGTAGTAAAAAGTAGCATGGCAGTTTCATAGTCTGTTT	1380
Db	1386	CTACAGTTTGAAGGCTATTTCTTGTAGTAAAAAGTAGCATGGCAGTTTCATAGTCTGTTT	1445
QY	1381	AAGTCTCTCTAGTGAAGACATATCAACTAAAAACAGAGATGAAATATTAAGGTGGGA	1440
Db	1446	AAGTCTCTCTAGTGAAGACATATCAACTAAAAACAGAGATGAAATATTAAGGTGGGA	1505
QY	1441	TGCGCTTTTGTAGTTGCTGTTAGTGGCAACCAACATTGAAGGAGTTTAAAGCTATATGTA	1500





920 ACAAACAAATTTAAGATAAATGATCTGCAAACTCTCTTTTAATGATGAAGATGAAA 979  
901 AATGTAATGGATTCCTCAAAATGACATTTCTGTAATACCTGGATCTATCTTCCCTCGACCA 960  
980 AATGTAATGGATTCCTCAAAATGACATTTCTGTAATACCTGGATCTATCTTCCCTCGACCA 1039  
961 GTAGAAATTTTAAACACAGTGACAGAAATCAGTTACAGTTATTTCAAGAAATGTAAGCACT 1020  
1040 GTAGAAATTTTAAACACAGTGACAGAAATCAGTTACAGTTATTTCAAGAAATGTAAGCACT 1099  
1021 AATGTCCTTCTCAAGCAACATGATTAATCATCATTTGAGTTTCTTTGATTTATCTACTGTCGTG 1080  
1100 AATGTCCTTCTCAAGCAACATGATTAATCATCATTTGAGTTTCTTTGATTTATCTACTGTCGTG 1159  
1081 AAGCCATCTCTCAACCTCAAGCAACATGATTAATCATCATTTGAGTTTCTTTGATTTATCTACTGTCGTG 1140  
1160 AAGCCATCTCTCAACCTCAAGCAACATGATTAATCATCATTTGAGTTTCTTTGATTTATCTACTGTCGTG 1219  
1141 ACTCTTGAAGAAAGAAAGAAATATGATGATCATTAACAGTGCACAGAGAACTATCTAG 1200  
1220 ACTCTTGAAGAAAGAAAGAAATATGATGATCATTAACAGTGCACAGAGAACTATCTAG 1279  
1201 TACTGGAGCGGATCTAACAGTGGAATCAGAAATGGAAGCTGTTTCAGAAAAATAAATAT 1260  
1280 TACTGGAGCGGATCTAACAGTGGAATCAGAAATGGAAGCTGTTTCAGAAAAATAAATAT 1339  
1261 ACTGTCCCAAGAGTGAACCTTTAAGATGAATTCCTCAATCCCAATCCTGAGGATTCAGTGAG 1320  
1340 ACTGTCCCAAGAGTGAACCTTTAAGATGAATTCCTCAATCCCAATCCTGAGGATTCAGTGAG 1399  
1321 CTACAGTTGAAGGCTTATTCCTTGTGTAGTAAAGTAGCATGCGAGTTCATAGTCTGTGTT 1380  
1400 CTACAGTTGAAGGCTTATTCCTTGTGTAGTAAAGTAGCATGCGAGTTCATAGTCTGTGTT 1459  
1381 AAGTCTCTAGTAAAGCATATACATCCAACTAAACCAAGAGATGAATAATTAAGGTGGGA 1440  
1460 AAGTCTCTAGTAAAGCATATACATCCAACTAAACCAAGAGATGAATAATTAAGGTGGGA 1512  
1441 TCGCCCTTTGAGTTGGTGTAGTGGCAACAAACGATTAAGGAGTTAAGCTATATGTTA 1500  
1513 -----GGTA 1516  
1501 GTATCCAGGGACAGTTGGTGTAGTGGCAACAAACGATTAAGGAGTTAAGCTATATGTTA 1560  
1517 GTATCCAGGGACAGTTGGTGTAGTGGCAACAAACGATTAAGGAGTTAAGCTATATGTTA 1576  
1561 CCAGAAATTTCTGGACTCCAAAGCCTGTAAATGTTGATTTATTTGAAGATGATGG 1620  
1577 CCAGAAATTTCTGGACTCCAAAGCCTGTAAATGTTGATTTATTTGAAGATGATGG 1636  
1621 GAAATTAAGTGAATGTTCTAAAAATTCCTGTTTCAAGCTTCTTTTAAAAATTAAGATAAG 1680  
1637 GAAATTAAGTGAATGTTCTAAAAATTCCTGTTTCAAGCTTCTTTTAAAAATTAAGATAAG 1696  
1681 CTATTTGGAGTAAAGTGAAGCTGAACCATCTGAGAAAGTCTCTTTAGGATCTCTGTG 1740  
1697 CTATTTGGAGTAAAGTGAAGCTGAACCATCTGAGAAAGTCTCTTTAGGATCTCTGTG 1756  
1741 ACACAGCTGACCTCAGTTGGATTTGAGTTGATGTTGACAAAAGTGTGAATCTGATGAAT 1800  
1757 ACACAGCTGACCTCAGTTGGATTTGAGTTGATGTTGACAAAAGTGTGAATCTGATGAAT 1816  
1801 GCCTCTAATGATTAATCAATGGAATGTTG 1830  
1817 GCCTCTAATGATTAATCAATGGAATGTTG 1846

RESULT 4  
US-10-264-237-1040  
; Sequence 1040, Application US/10264237  
; Publication No. US20040009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P431PI  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: Patent in Ver. 3.1  
; SEQ ID NO 1040  
; LENGTH: 1448  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-237-1040  
  
Query Match 23.7%; Score 1017; DB 16; Length 1448;  
Best Local Similarity 95.5%; Pred. No. 1.6e-255;  
Matches 1078; Conservative 0; Mismatches 0; Indels 51; Gaps 1;  
  
QY 3210 GTCATCCATTTTGGAGTCTGAATTCAGTAGAGGAATTCACACAATATATCTCTAGC 3269  
DB 1 GTCATCCATTTTGGAGTCTGAATTCAGTAGAGGAATTCACACAATATATCTCTAGC 60  
QY 3270 CTTTATACTTTATGCAATTCATCAGTGGGAGTCTTAAAGCGAAGGAAGCTTTGAATAT 3329  
DB 61 CTTTATACTTTATGCAATTCATCAGTGGGAGTCTTAAAGCGAAGGAAGCTTTGAATAT 120  
QY 3330 GCTGACTTGGAGAGAGAACAAAGAGGTGGCATGCAATTCCTGGTGTGATCAGAGTCCAA 3389  
DB 121 GCTGACTTGGAGAGAGAACAAAGAGGTGGCATGCAATTCCTGGTGTGATCAGAGTCCAA 180  
QY 3390 ACTTCTGACTCTCTGGGAGCCACGCTCCCTGGATATTAAGTTGACGCTATGCACTGCT 3449  
DB 181 ACTTCTGACTCTCTGGGAGCCACGCTCCCTGGATATTAAGTTGACGCTATGCACTGCT 240  
QY 3450 CTCACACTTCTTACAAATTCAGACTCTGAGGGAATCCCAATTTATGAGTGGCTAAGCAG 3509  
DB 241 CTCACACTTCTTACAAATTCAGACTCTGAGGGAATCCCAATTTATGAGTGGCTAAGCAG 300  
QY 3510 GCAAGAAATAGCTTGGTGGTGTTCATCTACTCAGATACCACTGTGGCTTTAAAGGC 3569  
DB 301 GCAAGAAATAGCTTGGTGGTGTTCATCTACTCAGATACCACTGTGGCTTTAAAGGC 360  
QY 3570 TCTGTCTGAATTTGAGCCCTTAATGAATACAGAAAGGACAAATATCCAAGTGACGTCAC 3629  
DB 361 TCTGTCTGAATTTGAGCCCTTAATGAATACAGAAAGGACAAATATCCAAGTGACGTCAC 420  
QY 3630 GGGGCTAGCTCACCAGTCTCTTAAAGTTCTGATTGACACACACCCGCTTACTCCT 3651  
DB 421 GGGGCTAGCTCACCAGTCTCTTAAAGTTCTGATTGACACACACCCGCTTACTCCT 480  
QY 3652 -----CTTGTGTGGTACAGCCCAATGGCAGTTAATATTTCCGCAAAATGGTTT 3698  
DB 481 TCAGACAGCAGAGCTTGTGTGGTACAGCCCAATGGCAGTTAATATTTCCGCAAAATGGTTT 540  
QY 3699 TGGATTGCTATTTCTCAGCTCAATGTTGTATATATGTAAGGCTTCTGGTCTTCTAG 3758  
DB 541 TGGATTGCTATTTCTCAGCTCAATGTTGTATATATGTAAGGCTTCTGGTCTTCTAG 600  
QY 3759 AAGACGAGATCTATCCAAATCAAGAGCCCTTGTATTAGATGTTGCTGTAAGAAAAA 3818  
DB 601 AAGACGAGATCTATCCAAATCAAGAGCCCTTGTATTAGATGTTGCTGTAAGAAAAA 660  
QY 3819 TAAAGATGATCTCAATCATGTTGAATTTGAATGTTGTAACAAGCTTTTCCGGCCCGGTAG 3878  
DB 661 TAAAGATGATCTCAATCATGTTGAATTTGAATGTTGTAACAAGCTTTTCCGGCCCGGTAG 720  
QY 3879 GAGTGGATGCTCTTATGAGGATTAACCTATTAGTGGCTTTATGCTTCAAGAGC 3938  
DB 721 GAGTGGATGCTCTTATGAGGATTAACCTATTAGTGGCTTTATGCTTCAAGAGC 780  
QY 3939 AATTTCTCTGAGGAGACAGTGAAGAAAGTGAATATGATCATGGAATACTCAACCTCTA 3998

D <sub>b</sub>	781	AATTTCTCTGAGCGAGACAGTGAAGAAGTGGAATATGATCATGGAAAACTCAACCTCTA	840
Q <sub>y</sub>	3999	TTTAGATTCTGTAAATGAACCAGTTTGTGTTTAATAATTCCTGCTGTGAGAAACTTTAA	4058
D <sub>b</sub>	841	TTTAGATTCTGTAAATGAACCAGTTTGTGTTTAATAATTCCTGCTGTGAGAAACTTTAA	900
Q <sub>y</sub>	4059	AGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATCAGGCCAAGGAGACA	4118
D <sub>b</sub>	901	AGTTTCAAATACCCAGATGCTTCAGTGTCCATAGTGGATTACTATCAGGCCAAGGAGACA	960
Q <sub>y</sub>	4119	GCGGGTCAGAAGTTACAACCTCTGAAGTGAAGCTGTCTCTCTGTGACCTTTGCAGTGAATG	4178
D <sub>b</sub>	961	GCGGGTCAGAAGTTACAACCTCTGAAGTGAAGCTGTCTCTCTGTGACCTTTGCAGTGAATG	1020
Q <sub>y</sub>	4179	CCAGGGCTCGCGTCTCTGTGAGGATGAGGCTTCAGGCTCCCATCATCACCTCTTCAGTCAT	4238
D <sub>b</sub>	1021	CCAGGGCTCGCGTCTCTGTGAGGATGAGGCTTCAGGCTCCCATCATCACCTCTTCAGTCAT	1080
Q <sub>y</sub>	4239	TTTTATTTTCTGTTTCAAGCTTCGTACTTTATGGAACCTTTGGCTGTGA	4287
D <sub>b</sub>	1081	TTTTATTTTCTGTTTCAAGCTTCGTACTTTATGGAACCTTTGGCTGTGA	1129

## RESULT 5

```

US-10-276-774-601/c
; Sequence 601, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 601
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-601

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Query Match	22.8%	Score	975.4	DB 13	Length	1459
Best Local Similarity	94.1%	Pred. No.	1.3e-244			
Matches 1078	Conservative	0	Mismatches	11	Indels	56
Gaps	4					
QY	3199	GATGTCGAAGAGCTATCCATTTTGGAGTCTGAAATTCAGTAGAGAAATTCAGACAAAT	3258			
Db	1455	GAGGTCGAAGAGCTCTCCATTTTGGAGTCTGAAATTCAGTAGAGAAATTCAGACAAAT	1396			
QY	3259	TATACCTTAGCCCTTATAACTTTATGCATTTGTCATCAGTGGGAGTCTTAAGCGAAGGAA	3318			
Db	1395	TATACCTTAGCCCTTATAACTTTATGCATTTGTCATCAGTGGGAGTCTTAAGCGAAGGAA	1336			
QY	3319	GCCTTCAATATGCTGACTTGGAGAGCAGACAGACAGAGGTGGCATGCAATCTCGGTCTCA	3378			
Db	1335	GCCTTCAATATGCTGACTTGGAGAGCAGACAGAGGTGGCATGCAATCTCGGTCTCA	1276			
QY	3379	TCAGAGTCCAAACTTTCTGACTCCTCGAGCCACGCTCCCTGGATATTGAAGTTGCAGCC	3438			
Db	1275	TCAGAGTCCAAACTTTCTGACTCCTCGAGCCACGCTCCCTGGATATTGAAGTTGCAGCC	1216			
QY	3439	TATGCACTGCTCCACACTTCTTACAAATTCAGACTTCTGAGGGAATCCCAATTATGAGG	3498			
Db	1215	TATGCACTGCTCCACACTTCTTACAAATTCAGACTTCTGAGGGAATCCCAATTATGAGG	1156			
QY	3499	TGCGTAAAGCAGGCAAGAAATAGCTTTGGGTGGTTTTGGCATCTACCTCAGGATACCACCTGTG	3558			

Db	1155	TGGCTAAGCAGGCAAGAAATAGCTTGGGTGGTTTTGGCATCTACTCAGGATACCACTGTG	1096
Qy	3559	GCTTTAAAGCCTCTGTCTGAATTTGCAGCCCTAATGAATA CAGAAAGGCAAAATATCCAA	3618
Db	1095	GC'TTTAAAGCCTCTGTCTGAATTTGCAGCCCTAATGAATACAGAAAGGCAAAATATCCAA	1036
Qy	3619	GTGACCGTGACGGGGCTAGCTCACCAAGTCCT-----	3651
Db	1035	GTGACCGTGACGGGGCTAGCTCACCAAGTCCTGTAAAGTTCTTGATTCGACACACACAC	976
Qy	3652	-----CTTGCTGTGGTACAGCCCAATGGCAGT-TAATATTT	3685
Db	975	CGCTTACTCTTTCAGACACAGAGACTTGTGTATGGTACAGCCCAATGGCAGTGTAAATTT	916
Qy	3686	CCGCAAAATGGTTTGGATTTGTCTATTTTGCAGCTCAATGTTGTATATAATGTGAAGCCTT	3745
Db	915	CCGCAAAATGGTTTGGATTTGTCTATTTTGCAGCTCAATGTTGTATATAATGTGAAGCCTT	856
Qy	3746	CTGGGTCTCTAGAGACGAGAGATCTATCCAAATCAAGAGCCTTTGTATTTAGATGTTG	3805
Db	855	CTGGGTCTCTAGAGACGAGAGATCTATCCAAATCAAGAGCCTTTGTATTTAGATGTTG	796
Qy	3806	CTGTAAAGAAAAATAAAGATGATCTCAATCATGTGGATTGGAATGTGTGACAAAGCTTTT	3865
Db	795	CTGTAAAGAAAAATAAAGATGATCTCAATCATGTGGATTGGAATGTGTGACAAAGCTTTT	736
Qy	3866	CGGGCCGGGTAGGATGGCATGGCTCTTATGGAAGTTAACCTTATTAAGTGGCTTTATGG	3925
Db	735	CGGGCCGGGTAGGATGGCATGGCTCTTATGGAAGTTAACCTTATTAAGTGGCTTTATGG	676
Qy	3926	TGCCTTTCAGAAGCAATTTCTCTGAGCGACAGCTGAAAGAAAGTGGAAATATGATCATGGAA	3985
Db	675	TGCCTTTCAGAAGCAATTTCTCTGAGCGACAGCTGAAAGAAAGTGGAAATATGATCATGGAA	616
Qy	3986	AATCAACCTCTATTTAGATCTGTAAATGAAACCCAGTTTGTGTATAATATCTGCTG	4045
Db	615	AATCAACCTCTATTTAGATCTGTAAATGAAACCCAGTTTGTGTATAATATCTGCTG	556
Qy	4046	TGAGAACTTTAAAGTTTCCAAATACCCAAGATGCTTTCAGTCCATAGTGGATTAATACTATG	4105
Db	555	TGAGAACTTTAAAGTTTCCAAATACCCAAGATGCTTTCAGTCCATAGTGGATTAATACTATG	496
Qy	4106	AGCCAGGAGACAGCGGTGAGAGTTACAACTCTGAGTGAAGCTGCTCCTCTGAGCC	4165
Db	495	AGCCAGGAGACAGCGGTGAGAGTTACAACTCTGAGTGAAGCTGCTCCTCTGAGCC	436
Qy	4166	TTTGCAAGTATGTCCAG-GGCTGCGGCTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCAT	4224
Db	435	TTTGCAAGTATGTCCAGAGGCTGCCGCTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCAT	376
Qy	4225	CACCTCTC--AGTCATTTTATTTCTGTGTTCAAGCTTCGTACTTTATGGAACCTTGGC	4282
Db	375	CACCTCTCAGTCGATTTTATTTCTGTGTTCAAGCTTCGTACTTTATGGAACCTTGGC	316
Qy	4283	TTTGA 4287	
Db	315	TTTGA 311	

## RESULT 6

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; RESULT: 6
; US-10-133-013-223
; Sequence 223, Application US/10133013
; Publication No. US20030165903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27

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QY 4166 TTTCAGTGATGTCAGGGCTGCCGCTCTGTGTAGGATGAGCTTCAGGCTCCATCATC 4225  
Db |||||  
435 TTTCAGTGATGTCAGGGCTGCCGCTCTGTGTAGGATGAGCTTCAGGCTCCATCATC 494  
QY 4226 ACTCTTCAGTCATTTTATTTCTTTCAAGCTTCTGTACTTTATGGAACCTTGGCTGT 4285  
Db |||||  
495 AMCTTCAGTCATTTTATTTCTTTCAAGCTTCTGTACTTTATGGAACCTTGGCTGT 554  
QY 4286 GA 4287  
Db |||  
555 GA 556

## RESULT 8

US-10-160-162-48  
; Sequence 48, Application US/10160162  
; Publication No. US20030166541A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 83 Human Secreted Proteins  
; FILE REFERENCE: P2012P2  
; CURRENT APPLICATION NUMBER: US/10/160,162  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: 60/295,558  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/236,557  
; PRIOR FILING DATE: 1999-01-26  
; PRIOR APPLICATION NUMBER: PCT/US98/15949  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: 60/054,212  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,209  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,234  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,218  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,214  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,236  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,215  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,211  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,217  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,213  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/055,968  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,969  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,972  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/056,561  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,534  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,729  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,543  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,727  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,554  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,730  
; PRIOR FILING DATE: 1997-08-19  
; NUMBER OF SEQ ID NOS: 353  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48

; LENGTH: 875  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-160-162-48  
  
Query Match 12.6%; Score 541.6; DB 15; Length 875;  
Best Local Similarity 99.8%; Pred. No. 6.8e-131;  
Matches 541; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3746 CTGGGTCTTCTAGAGACGAGATCTATCCAAATCAAGAGCCCTTTCATTAGATGTTG 3805  
Db |||||  
15 CTGGGTCTTCTAGAGACGAGATCTATCCAAATCAAGAGCCCTTTCATTAGATGTTG 74  
QY 3806 CTGTAAGAGAGAAATTAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTT 3865  
Db |||||  
75 CTGTAAGAGAGAAATTAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTT 134  
QY 3866 CGGGCCCGGTAGGATGGCTCTTATGGAAGTTAACTTAAAGTGGCTTTATG 3925  
Db |||||  
135 CGGGCCCGGTAGGATGGCTCTTATGGAAGTTAACTTAAAGTGGCTTTATG 194  
QY 3926 TGCCTTCAGAGCAATTTCTCTGAGCGAGACAGATGAAAGAAAGTGAATATGATCATGAA 3985  
Db |||||  
195 TGCCTTCAGAGCAATTTCTCTGAGCGAGACAGATGAAAGAAAGTGAATATGATCATGAA 254  
QY 3986 AACTCAACCTCTATTAGATTTCTGTAATGAACCCAGTTTGTGTTAAATTCCTGCTG 4045  
Db |||||  
255 AACTCAACCTCTATTAGATTTCTGTAATGAACCCAGTTTGTGTTAAATTCCTGCTG 314  
QY 4046 TGAGAACTTTAAAGTTTCAATACCAAGATGCTTCAGTGTCCATAGTGAATTAATG 4105  
Db |||||  
315 TGAGAACTTTAAAGTTTCAATACCAAGATGCTTCAGTGTCCATAGTGAATTAATG 374  
QY 4106 AGCCAAGGAGACAGCGCGTGAGAAAGTTACAACTCTGAAGTGAAGCTGTCTCTGTGACC 4165  
Db |||||  
375 AGCCAAGGAGACAGCGCGTGAGAAAGTTACAACTCTGAAGTGAAGCTGTCTCTGTGACC 434  
QY 4166 TTTCAGTGATGTCAGGGCTGCCGCTCTGTGTAGGATGAGCTTCAGGCTCCATCATC 4225  
Db |||||  
435 TTTCAGTGATGTCAGGGCTGCCGCTCTGTGTAGGATGAGCTTCAGGCTCCATCATC 494  
QY 4226 ACTCTTCAGTCATTTTATTTCTTTCAAGCTTCTGTACTTTATGGAACCTTGGCTGT 4285  
Db |||||  
495 AMCTTCAGTCATTTTATTTCTTTCAAGCTTCTGTACTTTATGGAACCTTGGCTGT 554  
QY 4286 GA 4287  
Db |||  
555 GA 556

## RESULT 9

US-10-211-462-208  
; Sequence 208, Application US/10211462  
; Publication No. US2004003495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murrain, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29

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; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-462-208

Query Match
Best Local Similarity 12.2%; Score 525; DB 13; Length 821;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3763 CGAAGATCTATCAAAATCAAGAGCTTTGATTAGATGCTGCTCTAAAGAAATAAA 3822
Db 1 CGAAGATCTATCAAAATCAAGAGCTTTGATTAGATGCTGCTCTAAAGAAATAAA 60

QY 3823 GATGATCTCAATCATGTGGATTTGAATGTGTGTACAAAGCTTTTCGGGCCCGGTAGAGT 3882
Db 61 GATGATCTCAATCATGTGGATTTGAATGTGTGTACAAAGCTTTTCGGGCCCGGTAGAGT 120

QY 3883 GGCATGGCTCTTATGGAAGTTAACCTATTAAAGTGGCTTTATGCTGCTTCAGAAGCAAT 3942
Db 121 GGCATGGCTCTTATGGAAGTTAACCTATTAAAGTGGCTTTATGCTGCTTCAGAAGCAAT 180

QY 3943 TCTCTGAGCAGACAGTGAAGAAAGTGAATATGATCATGGAATAACTCAACCTCTATTTA 4002
Db 181 TCTCTGAGCAGACAGTGAAGAAAGTGAATATGATCATGGAATAACTCAACCTCTATTTA 240

QY 4003 GATTCGTAAATGAACCCAGTTTGTGTTAAATTCCTGCTGTGAGAACTTTAAAGTT 4062
Db 241 GATTCGTAAATGAACCCAGTTTGTGTTAAATTCCTGCTGTGAGAACTTTAAAGTT 300

QY 4063 TCAATACCCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAAGGACAGGCG 4122
Db 301 TCAATACCCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAAGGACAGGCG 360

QY 4123 GTGAGAAGTTACAACCTGTAAGTGAAGCTCTCTCTGTGACCTTTGCGATGATGCCAG 4182
Db 361 GTGAGAAGTTACAACCTGTAAGTGAAGCTCTCTCTGTGACCTTTGCGATGATGCCAG 420

QY 4183 GCGTCGCGCTCTGTGAGGATGGAGCTTCAGGCTCCCATCATCAGCTTCAGTCATTTT 4242
Db 421 GCGTCGCGCTCTGTGAGGATGGAGCTTCAGGCTCCCATCATCAGCTTCAGTCATTTT 480

QY 4243 ATTTTCTGTTTCAAGCTTCTGACTTTATGGAACCTTTGGCTGTGA 4287
Db 481 ATTTTCTGTTTCAAGCTTCTGACTTTATGGAACCTTTGGCTGTGA 525

RESULT 10
US-10-085-783A-45412
; Sequence 45412, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45412
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-45412

Query Match
Best Local Similarity 11.6%; Score 497.4; DB 16; Length 520;
Matches 509; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2872 AGGCAAGGTTACCA-GAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAAGTCTTT 2930
Db 1 AGGCAAGGTTACCAATGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAAGTCTTT 60

QY 2931 TGGGAATATGACCCCTTCTGGAGCACTTGGTGTGACCTTTGTTTAAAGATGTTTCT 2990
Db 61 TGGGAATATGACCCCTTCTGGAGCACTTGGTGTGACCTTTGTTTAAAGATGTTTCT 120

QY 2991 TGAAGCCGATCCTTACATAGATATTGATCAGAATGTGTTACACAGAAATACACACTTGGCT 3050
Db 121 TGAAGCCGATCCTTACATAGATATTGATCAGAATGTGTTACACAGAAATACACACTTGGCT 180

QY 3051 TAAAGCAATCAGAAATCCAAACGGTGAATTTTGGATCCAGGAAGAGTATCATAGTGA 3110
Db 181 TAAAGCAATCAGAAATCCAAACGGTGAATTTTGGATCCAGGAAGAGTATCATAGTGA 240

QY 3111 GCTTCAAGTGGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACCTTCTCTCT 3170
Db 241 GCTTCAAGTGGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACCTTCTCTCT 300

QY 3171 GGGATATAGAAGTATACGCTTAACATTCATGTGCAAGAGTCTATCCATTTTGGAGTC 3230
Db 301 GGGATATAGAAGTATACGCTTAACATTCATGTGCAAGAGTCTATCCATTTTGGAGTC 360

QY 3231 TGAATTCAGTAGAGAAATTCAGACAATATATCTAGCCCTTATACCTTATGCAATTCG 3290
Db 361 TGAATTCAGTAGAGAAATTCAGACAATATATCTAGCCCTTATACCTTATGCAATTCG 420

QY 3291 ATCACTGGGAGTCCCTAAAGGGAAGAGCTTGAATATGCTGACTTGGAGAGCAGAAACA 3350
Db 421 ATCACTGGGAGTCCCTAAAGGGAAGAGCTTGAATATGCTGACTTGGAGAGCAGAAACA 480

QY 3351 AGAAGTGGCATGCAATCTCGGTGTCATCA 3391
Db 481 AGAAGTGGCATGCAATCTCGGTGTCATCA 511

RESULT 11
US-10-242-535A-45412
; Sequence 45412, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45412
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-45412

Query Match
Best Local Similarity 99.6%; Pred. No. 1.8e-119;
Matches 509; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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2872	QY	AGGCAAGGTTACCA-GAGAGAACTTCTCTATCAGAGGGAAGATGCTCTTTCAGTGCTTT	2930
1	Db	AGGCAAGGTTACCAATGAGAACTTCTCTATCAGAGGGAAGATGCTCTTTCAGTGCTTT	60
2931	QY	TGGGAATTATGACCCCTCTCGGAGACACTTGGTTGTGAGCTTTTGTTTAAGATGTTTCCT	2990
61	Db	TGGGAATTATGACCCCTCTCGGAGACACTTGGTTGTGAGCTTTTGTTTAAGATGTTTCCT	120
2991	QY	TGAAGCCGATCCTTACATAGATATTGATCAGAAATGTGTTACACAGAAATACACTTGGCT	3050
121	Db	TGAAGCCGATCCTTACATAGATATTGATCAGAAATGTGTTACACAGAAATACACTTGGCT	180
3051	QY	TAAAGGACATCAGAAATCCAAACGGTCAATTTTGGGATCCAGGAAGAGTGATTTCATAGTGA	3110
181	Db	TAAAGGACATCAGAAATCCAAACGGTCAATTTTGGGATCCAGGAAGAGTGATTTCATAGTGA	240
3111	QY	GCCTCAAGGTGGCAATAAAAGTCCAGTAACTATACAGCCCTAATATTGTAACCTTCTCCT	3170
241	Db	GCCTCAAGGTGGCAATAAAAGTCCAGTAACTATACAGCCCTAATATTGTAACCTTCTCCT	300
3171	QY	GGGATATAGAAGTGATCAGGCTTAACATTCGATGTGAAGAGTCTATCCATTTTTTGGAGTC	3230
301	Db	GGGATATAGAAGTGATCAGGCTTAACATTCGATGTGAAGAGTCTATCCATTTTTTGGAGTC	360
3231	QY	TGAATTCAGTAGAGGAATTTACAGCAATATATCTTAGCCCTTATAACTTATGCAATTGTC	3290
361	Db	TGAATTCAGTAGAGGAATTTACAGCAATATATCTTAGCCCTTATAACTTATGCAATTGTC	420
3291	QY	ATCAGTGGGAGTCTCTAAACGGGAAGAAAGCTTTGAATATGCTGACTTGGAGAGCAGAAACA	3350
421	Db	ATCAGTGGGAGTCTCTAAACGGGAAGAAAGCTTTGAATATGCTGACTTGGAGAGCAGAAACA	480
3351	QY	AGAAGGTGGCAATGCAATTCCTGGGTGTCATCA	3381
481	Db	AGAAGGTGGCAATGCAATTCCTGGGTGTCATCA	511

## RESULT 12

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Result 12
US-10-085-783A-29628
; Sequence 29628, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING-DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29628
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (41)..(41)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:

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QY 3760 AGACGAGATCTATCCAAATCAAGAGCCTTTGATTAGTCTGCTGTAAGA 3815
Db 444 AGACGAGATCTATCCAAATCAAGAGCCTTTGATTAGTCTGCTGTAAGA 499

RESULT 13
US-10-242-535A-29628
; Sequence 29628, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29628
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (41)..(41)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (50)..(50)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)..(59)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(92)
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; FEATURE:
; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
; LOCATION: (122)..(122)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (130)..(130)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (182)..(182)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (190)..(190)
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (412)..(412)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-29628

Query Match 7.8%; Score 334.8; DB 16; Length 499;
Best Local Similarity 84.7%; Pred. No. 8.6e-77;
Matches 403; Conservative 0; Mismatches 22; Indels 51; Gaps 1;

QY 3391 CTTTCTGACTCCTGGCAGCCAGCGTCCCTGCATATTGAAGTTGCAGCTATGCACTGCTC 3450
Db 24 CTTCTAATACAGAGCAGCCAGCTCCTGATATGAAGCTATGCACTGCTC 83
QY 3451 TCACACTTCTTACAAATTCAGACTTCTGAGGGAATCCCAATTATGAGTGGCTAAGCAGG 3510
Db 84 TCACACTTNTTACAATNTCAGACTTCTGAGGGAATCCCNATTATGANGTGGCTAAGCAGG 143
QY 3511 CAAGAAATAGCTTGGGTGGTGGTTCATCTACTCAGGATACCATCTGGCTTTAAAGGCT 3570
Db 144 CAAGAAATAGCTGGGTGGTGGTTCATCTACTCAGGATACCATCTGGCTTTAAAGGCT 203
QY 3571 CTGTCTGAATTTGCAGCCCTAATGAATACAGAAAGGACAAATATCCCAAGTACCGTGCAG 3630
Db 204 CTGTCTGAATTTGCAGCCCTAATGAATACAGAAAGGACAAATATCCCAAGTACCGTGCAG 263
QY 3631 GGGCTAGCTCACCAGTCTCT----- 3651
Db 264 GGGCTAGCTCACCAGTCTCTGTTNAAGTTTCTGATTGACACACACACCGCTTACTCTCTT 323
QY 3652 -----CTTGTGTGTACAGCCATGCGCAGTATATATTCGCAAAATGGTTT 3699
Db 324 CAGACAGCAGAGCTGTGTGTACAGCCAAATGGCAGTAAATATTCGCAAAATGGTTT 383
QY 3700 GGATTTGCTATTGTTCAGCTCAATGTTGTATATATATGAGGCTTCTGGTCTTCTAGA 3759
Db 384 GGATTTGCTATTGTTCAGCTCAATGTTGNATATATATGAGGCTTCTGGTCTTCTAGA 443
QY 3760 AGACGAGATCTATCCAAATCAAGAGCCTTTGATTAGTCTGCTGTAAGA 3815
Db 444 AGACGAGATCTATCCAAATCAAGAGCCTTTGATTAGTCTGCTGTAAGA 499

RESULT 14
US-10-085-783A-46128
; Sequence 46128, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46128
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (49)..(49)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-085-783A-46128

Query Match  
Best Local Similarity 98.7%; Score 297.2; DB 13; Length 303;  
Matches 299; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 521 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGTGCATCTTGGAGTCATTTCCAAAACCTTTTC 580  
Db 1 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGAGATCTTGGAGTCATTTNCAAAACCTTTTC 60  
QY 581 AGTATATCTCCCAATCCCAATCTTGGTACTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 640  
Db 61 AGCTATCTCCCAATCCCAATCTTGGAGTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 120  
QY 641 CATATATCAATCAATCTTCCAGTTTTCAGATATGATATACCATAATTTGAAGTGACTTTGC 700  
Db 121 CATACTATCAATCAATCTTCCAGTTTTCAGATATGATATACCATAATTTGAAGTGACTTTGC 180  
QY 701 AGACACCATTTATATTTCTATGAATTTCTAAGCATTTAAATGGTACCATCACGGCAAAGT 760  
Db 181 AGACACCATTTATATTTCTATGAATTTCTAAGCATTTAAATGGTACCATCACGGCAAAGT 240  
QY 761 ATACATATGGGAAGCCAGTGAAGGAGACGTAACGCTTACATTTTACCTTTATCCCTTTT 820  
Db 241 ATACATATGGGAAGCCAGTGAAGGAGACGTAACGCTTACATTTTACCTTTATCCCTTTT 300  
QY 821 GGG 823  
Db 301 GGG 303

## RESULT 15

US-10-242-535A-46128  
; Sequence 46128, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 46128  
; LENGTH: 303  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (49)..(49)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-242-535A-46128

Query Match  
Best Local Similarity 98.7%; Score 297.2; DB 16; Length 303;  
Matches 299; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 521 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGTGCATCTTGGAGTCATTTCCAAAACCTTTTC 580  
Db 1 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGAGATCTTGGAGTCATTTNCAAAACCTTTTC 60  
QY 581 AGCTATCTCCCAATCCCAATCTTGGTACTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 640

Db 61 AGCTATCTCCCAATCCCAATCTTGGAGACTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 120  
QY 641 CATATATCAATCAATCTTCCAGTTTTCAGATATGATATACCATAATTTGAAGTGACTTTGC 700  
Db 121 CATACTATCAATCAATCTTCCAGTTTTCAGATATGATATACCATAATTTGAAGTGACTTTGC 180  
QY 701 AGACACCATTTATATTTCTATGAATTTCTAAGCATTTAAATGGTACCATCACGGCAAAGT 760  
Db 181 AGACACCATTTATATTTCTATGAATTTCTAAGCATTTAAATGGTACCATCACGGCAAAGT 240  
QY 761 ATACATATGGGAAGCCAGTGAAGGAGACGTAACGCTTACATTTTACCTTTATCCCTTTT 820  
Db 241 ATACATATGGGAAGCCAGTGAAGGAGACGTAACGCTTACATTTTACCTTTATCCCTTTT 300  
QY 821 GGG 823  
Db 301 GGG 303

Search completed: August 18, 2004, 05:25:37  
Job time : 2200 secs



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OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 23:19:30 ; Search time 277 Seconds  
(without alignments)  
8588.717 Million cell updates/sec

Title: US-10-020-095-3  
 Perfect score: 4287  
 Sequence: 1 atcgagggccaccacctctt.....ttatcgaaattttggtctatga 4287

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2584.6	60.3	3033	4	US-09-833-381-1810	Sequence 1810, Ap
2	110	2.6	4079	4	US-09-016-434-1174	Sequence 1174, Ap
3	110	2.6	4577	4	US-09-241-606-1	Sequence 1, Appli
4	108.4	2.5	4792	4	US-09-566-921-109	Sequence 109, App
5	49	1.1	832	4	US-09-621-976-2813	Sequence 2813, Ap
C 6	47.4	1.1	7218	1	US-08-232-463-14	Sequence 14, Appli
7	47.2	1.1	339	4	US-09-311-352B-1	Sequence 1, Appli
8	46.4	1.1	5211	1	US-08-447-411-1	Sequence 1, Appli
9	45.4	1.1	2802	4	US-09-976-594-924	Sequence 924, App
10	44	1.0	333	4	US-09-241-606-5	Sequence 5, Appli
11	44	1.0	750	4	US-09-241-606-3	Sequence 3, Appli
C 12	42.8	1.0	832	4	US-09-621-976-2813	Sequence 2813, Ap
C 13	41.6	1.0	10467	4	US-10-204-708-2	Sequence 2, Appli
14	41.4	1.0	5398	3	US-09-356-952-11	Sequence 11, Appli
C 15	41.4	1.0	1664976	4	US-09-916-421B-1	Sequence 1, Appli
16	40.2	0.9	657	4	US-09-134-000C-865	Sequence 865, App
17	40	0.9	1581	4	US-09-601-198-80	Sequence 80, Appli
C 18	39.4	0.9	15016	4	US-09-601-198-60	Sequence 60, Appli
C 19	38.8	0.9	1327	4	US-09-350-758-9	Sequence 9, Appli
C 20	38.8	0.9	3981	2	US-08-955-138-2	Sequence 2, Appli
21	38.6	0.9	1579	4	US-09-071-035-83	Sequence 83, Appli
C 22	38.6	0.9	1680	4	US-09-071-035-81	Sequence 81, Appli
23	38.2	0.9	3027	4	US-09-328-352-3277	Sequence 3277, Ap
C 24	38.2	0.9	540881	4	US-09-790-988-1	Sequence 1, Appli
25	38	0.9	399	4	US-09-621-976-8976	Sequence 8976, Ap
C 26	38	0.9	30549	4	US-09-134-001C-322	Sequence 322, App
C 27	37.8	0.9	474	4	US-09-621-976-18033	Sequence 18033, A

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RESULT 1
US-09-833-381-1810
SEQUENCE 1810, Application US/09833381
Patent No. 6672186
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic A
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/515,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1810
LENGTH: 3033
TYPE: DNA
ORGANISM: Homo sapiens
US-09-833-381-1810

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### Query Match

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Query Match          60.3%; Score 2584.6; DB 4; Length 3033;
Best Local Similarity 98.0%; Pred. NO. 0;
Matches 2648; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

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1636	QY	GTCTAAAAATTCCTGCTTACCTGTGTTTTTAAAAATTAAGATAAAGCTATATTGGAGTAAA	1695
	Db	GTCCGAAAAATTCCTGCTTACCTGCTGTTTTTAAAAATTAAGATAAAGCTATATTGGAGTAAA	65
1696	QY	GTGAAGCTGAACCATCTGAGAAAGTCTCTCTTAGATCTCTGTACACAGCCGTGACTCC	1755
66	Db	GTGAAGCTGAACCATCTGAGAAAGTCTCTCTTAGATCTCTGTACACAGCCGTGACTCC	125
1756	QY	ATATGTTGGGATTGTAGCTGTGTGACAAAAGTGAATCTGATGAATCCCTCTTAATGATATT	1815
126	Db	ATATGTTGGGATTGTAGCTGTGTGACAAAAGTGAATCTGATGAATCCCTCTTAATGATATT	185
1816	QY	ACATGAGAAATGTGTCCTAGTTGGAACTTTATAACACAGGATATATTATTGGCGATG	1875
186	Db	ACATGAGAAATGTGTCCTAGTTGGAACTTTATAACACAGGATATATTATTGGCGATG	245
1876	QY	TTCATGAATTCCTTTGCGAGTCTTTTCAGGAATGTGGAATCTCGGATATTGACAGATGCAAC	1935
246	Db	TTCATGAATTCCTTTGCGAGTCTTTTCAGGAATGTGGAATCTCGGATATTGACAGATGCAAC	305
1936	QY	CTCAGGAAGTATATATTGATGGTGTTTATGCAATGCAGATATGCTGAGAGGTTTATG	1995
306	Db	CTCAGGAAGTATATATTGATGGTGTTTATGCAATGCAGATATGCTGAGAGGTTTATG	365
1996	QY	GAGGAAAATGAAGACATATTGTAGATATTTCATGCTTTTCTTGGGTAGCAGTCCACAT	2055

Db	366	GAGGAAATGAAGGACATATTGTAGATATTCTATGACCTTTCTTTGGTAGCAGTCACAT	425
Qy	2056	GTCCGAAGACATTTTCCAGAGACTTGGATTTGGCTAGACACCAACATGGGTTACAGGATT	2115
Db	426	GTCCGAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAACATGGGTTACAGGATT	485
Qy	2116	TACCAAGAAATTGAAGTAACTGTACCTGATTTCTATCATCTTCTTTGGGTGGCTACTGGTTT	2175
Db	486	TACCAAGAAATTGAAGTAACTGTACCTGATTTCTATCATCTTCTTTGGGTGGCTACTGGTTT	545
Qy	2176	GTGATCTCTCAGGACCTGGGCTTTGGACTAACCAACTACTCCAGTGGAGTCTCAAGGCTTTC	2235
Db	546	GTGATCTCTCAGGACCTGGGCTTTGGACTAACCAACTACTCCAGTGGAGTCTCAAGGCTTTC	605
Qy	2236	CAACCATTTTTCATTTTTTTGAATCTTCCCTACTCTGTATTACAGAGGTGAAGAAATTGCT	2295
Db	606	CAACCATTTTTCATTTTTTTGAATCTTCCCTACTCTGTATTACAGAGGTGAAGAAATTGCT	665
Qy	2296	TTGGAAATAACTATATTCAATTAATTTCAAAGATGCCACTGAGGTTAAGGTAAATCAATTGAG	2355
Db	666	TTGGAAATAACTATATTCAATTAATTTGAAGAATGCCACTGAGGTTAAGGTAAATCAATTGAG	725
Qy	2356	AAAAGTGACAAAATTGTATATTCTAATGACTTCAAGTGAATAAATGCCACAGGCCACCAG	2415
Db	726	AAAAGTGACAAAATTGTATATTCTAATGACTTCAAAATGAAATGAAATGCCACAGGCCACCAG	785
Qy	2416	CAGACCCTTCTGGTCCCACTGAGGATGGGCACTGTTCTTTTCCATCGCCCAACA	2475
Db	786	CAGACCCTTCTGGTCCCACTGAGGATGGGCACTGTTCTTTTCCATCGCCCAACA	845
Qy	2476	CACTCGGAGAAAATTCCTATCACAGTCACAGCTCTTTTCCACCACTGCTCTGTAGTCTGTC	2535
Db	846	CACTCGGAGAAAATTCCTATCACAGTCACAGCTCTTTTCCACCACTGCTCTGTAGTCTATC	905
Qy	2536	ACCAGATGATTTTGTATTAAGGCTGAAGGAATAGAAAATCATATTCACAAATCCATCTTA	2595
Db	906	ACCAGATGATTTTGTATTAAGGCTGAAGGAATAGAAAATCATATTCACAAATCCATCTTA	965
Qy	2596	TTAGACTTGACTGCAATAGGCTACAGATACCTCGAAAACCTTTGAGTTTCTCATTTTCTT	2655
Db	966	TTAGACTTGACTGCAATAGGCTACAGATACCTCGAAAACCTTTGAGTTTCTCATTTTCTT	1025
Qy	2656	CCTAATACAGTACTGCGAGTGAAGAGTTCAGATCACTGCAATTTGGAGATGTTCTTGGT	2715
Db	1026	CCTAATACAGTACTGCGAGTGAAGAGTTCAGATCACTGCAATTTGGAGATGTTCTTGGT	1085
Qy	2716	CTTTCATCAATGGCTTAGCTCATTCGATGCGATGCTTATGGCTGTGTGAACAGAAC	2775
Db	1086	CTTTCATCAATGGCTTAGCTCATTCGATGCGATGCTTATGGCTGTGTGAACAGAAC	1145
Qy	2776	ATGATAAATTTTGTCTCCAAATATTACATTTTGGATTATCTGACTAAAAAGAACAACTG	2835
Db	1146	ATGATAAATTTTGTCTCCAAATATTACATTTTGGATTATCTGACTAAAAAGAACAACTG	1205
Qy	2836	ACAGATAATTGAAGAAAAGCTCTTTCATTTATGAGGCAAGGTTACACAGAGAGACTT	2895
Db	1206	ACAGATAATTGAAGAAAAGCTCTTTCATTTATGAGGCAAGGTTACACAGAGAGACTT	1265
Qy	2896	CTCTATCAGAGGGAAGATGGCTCTTTTCAGTGTCTTTTGGGAATTATGACCCCTCTGGGAGC	2955
Db	1266	CTCTATCAGAGGGAAGATGGCTCTTTTCAGTGTCTTTTGGGAATTATGACCCCTCTGGGAGC	1325
Qy	2956	ACTTGGTTGTGAGCTTTTGTTTTAAAGATGTTTCTTGAAGCCGATCCTTACATAGATATT	3015
Db	1326	ACTTGGTTGTGAGCTTTTGTTTTAAAGATGTTTCTTGAAGCCGATCCTTACATAGATATT	1385
Qy	3016	GATCAGAAATGTGTTTACAGAAACATACACTTGGCTTAAAGACATCAGAAATCCACCGT	3075
Db	1386	GATCAGAAATGTGTTTACAGAAACATACACTTGGCTTAAAGACATCAGAAATCCACCGT	1445
Qy	3076	GAATTTTGGATCCAGGAAGATGATTCATAGTGAGCTTCAAGGTGGCAATAAAGTCCA	3135
Db	1446	GAATTTTGGATCCAGGAAGATGATTCATAGTGAGCTTCAAGGTGGCAATAAAGTCCA	1505

2769	ACAGAACATGATAAAATTTTGCCTCCAAATATTTACATTTTGGATTATCTGACTAAAAAGAA	2828
2965	GCAGAAATATGGTCCTCTTTTGCCTCTTAAACATCTATGTACTGGATTATCTAAATGAACACAC	3024
2829	ACAACCTGACAGATAATTTCAAAGAAAAAGCTCTTTTCATTTATGAGGCAAGGTTTACCAGAG	2888
3025	GCAGCTTACTCCAGAGGTCAGTCCAGGCCATTGGCTATCTCAACACTGGTTTACCAGAG	3084
2889	AGAACTTCTCTATCAGAGGGAAGATGGCTCTTTTCAGTGTCTTTTGGG-----AATTATGA	2942
3085	ACAGTTGAACTACAAACACTATGATGGCTCTCTACAGCACTTTGGGAGCGGATATGGCAG	3144
2943	CCCTCTCTGGAGCACCTTGGTGTGTCAGCTTTTCTGTTTAAAGATGTTTCTCTTGAAGCCGATCC	3002
3145	GAACAGGSCAACACCTGGCTCACAGCCTTGTCTGAAGACTTTTGCCCAAGCTCGAGC	3204
3003	TTACATAGATATTGATCAAGATGTGTTACACAGAACATACACTTGGCTTTAAAGGACATCA	3062
3205	CTACATCTTTATCGATGAAGCACACATTACCACAGCCCTCATATGGCTCTCCACAGAGGCA	3264
3063	GAATCCACCGTGAATTTTGGATCCAGGAGAGTGATTCATAGTGAGCTTTCAGGTTG	3122
3265	GAAGACAAATGGCTGTTTCAGAGAGCTCTGGGTCACTGCTCAACAATGCCAATAAGGGAGG	3324
3123	CAATAAAAGTCCAGTAACACTTACAGCCCTATATTGTACTTCTCTCTGGGATATAGAAA	3182
3325	AGTAGAAGATGAAGTGACCCCTCTCGGCTATATACCACTCGCCCTTCGAGATTCCCTCT	3384
3183	GTATCAGCCTACATTTGATGTCGAAGAGTCTATCCATTTTTCGGAGTCTGAATTCAGTAG	3242
3385	CACAGTCACTCAACCCTGTTGTCCGCAATGCCCTGTTTTCCTGGAGTCAGCCTGGAAGAC	3444
3243	AGGA	3246
3445	AGCA	3448

### RESULT 3

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RESULT 3
US-09-241-606-1
; Sequence 1, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Alister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4450003
; CURRENT APPLICATION NUMBER: US/09/241,606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (44)..(112)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)..(4468)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (113)..(4468)
US-09-241-606-1

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Query Match 2.6%; Score 110; DB 4; Length 4577;  
Best Local Similarity 50.2%; Pred. No. 4e-21;  
Matches 303; Conservative 0; Mismatches 295; Indels 6; Gaps 1;  
2649 ATTTCCTCCCTAATACAGTGTGTCAGTGAAGAGAGTTTCAGATCACTCAATTTGGAGATGT 2708



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QY 2890 GAACCTCTCTCATGAGAGGAGATGGCTCTTTCAGTGCCTTTTGGGAATTATGACCCCTTCT 2949
Db 61 RYANWGTYKKKAMCRITKXKKKKGYMMWYGMRRSYNAWTRTWGYAYYRSMYWMR 120
QY 2950 GGGAGCACCTTGGTTGTGAGCTTTTGTGTTTAAAGATGTTTCCCTTGAAGCCGATCCTTTACATA 3009
Db 121 YRCWKKAYRKTTTCYSSKGNWKRKKXAWTTWWKKTYNAATRWMMWMTKWRAS 180
QY 3010 GATATTGATCAGATGTGTTACAGAGACATACACITGGCTTAAAGGACATCAGAAATCC 3069
Db 181 WYCWMMWKGARKNWTWRKRSYASARSAKCCYSCSWGAMSWKYMWMWWRGWATGAGM 240
QY 3070 AACGGTGAATTTTGGGATCCAGGAAGAGTGAATTCATAGTGAGCTTCAAGGTGGCAATAAA 3129
Db 241 KAWRASCMWRKYGAKSKTSYKSMWMCWTRSWKYCYTKARWTGYCYVRKGMWKGKGRWY 300
QY 3130 AGTCCAGTAACTTACAGCTTATGTTAACTTCTCTCTCGGATATAGAAAGTATCA 3188
Db 301 ASKKYMKRWMMWCMWARMYRSTGTIRASMMWRRTYTTMMKWKWKYAWARAARWMMWA 359

RESULT 6
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fis
; US-08-232-463-14

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Query Match          1.1%; Score 47.4; DB 1; Length 7218;
Best Local Similarity 4.5%; Pred. No. 0.01;
Matches 18; Conservative 217; Mismatches 169; Indels 0; Gaps 0;
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Qy	1149	AGAAAGAAGAATAATAGTGTAGTCAATACAGTGACACAGAGAACTATACTAGTACTGGAG	1209
Db	1457	AAAGAGATGAAGAAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1398
Qy	1209	CGGATCTCAACAGTGGAAATCAGAAAAATGGAAGCTGTTTCAGAAAAATAAATATATACTGTCCC	1268
Db	1397	RR	1338
Qy	1269	CMAAGTGAACCTTTTAAGATGGAATCCCAATCCTGGAGGATTCAGTGAGCTACAGTT	1328
Db	1337	RR	1278
Qy	1329	GAAGGCGCTATTTCTCTGGTAGTAAAAAGTAGCATGGCAGTTTCATAGTCTGTTTAAGTCTCC	1388
Db	1277	RR	1218
Qy	1389	TAGTAAACATACATCACTAAACAAACAGAGATGAAATATAAAGTGGGATCGCCTTT	1448
Db	1217	RR	1158
Qy	1449	TGAGTTGGTGGTTAGTGGCAACAAACGATTAAGAGGAGTTAAAGCTATATGTAGTATCCAG	1508
Db	1157	RR	1098
Qy	1509	GGGACAGTTGGTGGCTGTAGGAAAAACAAATTCACAAATGCTC	1551
Db	1097	RR	1055

RESULT 7

US-09-311-352B-1

; Sequence 1, Application US/09311352B  
; Patent No. 6329500  
; GENERAL INFORMATION:  
; APPLICANT: Webb, Donna J.  
; APPLICANT: Gonias, Steven L.  
; TITLE OF INVENTION: Transforming Growth Factor-beta Binding Site  
; FILE REFERENCE: 00370-02  
; CURRENT APPLICATION NUMBER: US/09/311,352B  
; CURRENT FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-311-352B-1

Query Match

Best Local Similarity 53.0%; Pred.No.0.0013;

Matches 125; Conservative 0; Mismatches 108; Indels 3; Gaps 1;

Qy	2056	GTCCGAAAGCATTTTCCAGAGACTTCGATTTGGCTAGACACCAACATGGGTTACAGGATT	2115
Db	97	GTAGGAAGTACTTCCCTGNAGACATGATCTGGGATTTGGTGGTAACTCAGCAGGG	156
Qy	2116	TACCAAGAATTTGAAGTAATGTAAGTCTGATTTCTATCACTTTTGGTGGGCTACTGGTTTT	2175
Db	157	GTGGCTCAGTAGGAGTAACAGTCCCTGACACCATCACCGAGTGGGAAGGCAGGGCGCTTC	216
Qy	2176	GTGATCTCTGAGGACCTGGTCTTTGGACTAAACAACTACTCCAGTGGAGCTCCCAAGCCTTC	2235
Db	217	TGCGCTGTCTGAAGATGCTGGAATTTGTATCTCTTCACATGCGCTCTCTCTCCCGAGCCTTC	273
Qy	2236	CAACCAATTTTCAATTTTTTTTGAATCTTCCTACTCTGTGTATCAAGGTGAAGATT	2291
Db	274	CAGCCCTCTTTTGTGGAGTCAAAATGCCTTACTCTGTGATCTCTGTGAGAGGCTT	329

RESULT 8  
US-08-447-411-1  
; Sequence 1, Application US/08447411

Patent No. 5773243  
 GENERAL INFORMATION:  
 APPLICANT: FRITZINGER, DAVID C.  
 APPLICANT: BREDEHORST, REINHARD  
 APPLICANT: VOGEL, CARL-WILHELM  
 TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
 ADDRESSEE: P.C.  
 STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/447,411  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/043,747  
 FILING DATE: 07-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Oblon, No. 5773243man P.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 1126-101-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5211 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 9..4961  
 US-08-447-411-1

Query Match 1.1%; Score 46.4; DB 1; Length 5211;  
 Best Local Similarity 50.4%; Pred. No. 0.016;  
 Matches 113; Conservative 0; Mismatches 111; Indels 0; Gaps 0;  
 QY 3376 TCATCAGAGTCCAACTTCTGACTCCTGCGACGCCAGCTCCCTGGATATTGAAGTTGCA 3435  
 Db 3609 TCAACAGGAGGAATCGTTGGGAAGATATATGCTCGCACCCATATATTTGAAGGCACT 3668  
 QY 3436 GCCTATGCTGCTCTCAGACTTCTTACATTTTCAGACTTCTGAGGGAATCCCAATTATG 3495  
 Db 3669 TCTATGCTTGTGTGGCCCTGCTGAATAATGAAGAAATTTGCTGAGTCCGCTCTGTATGTC 3728  
 QY 3496 AGGTGGCTACAGGCAAGAAATAGCTTGGTGGTGTTCATCTACTCAGGATACCACT 3555  
 Db 3729 AGATGGCTGATAGATCAGAAATATTATGGGGAAACATATGGACAAACCCCAAGCAAGTT 3788  
 QY 3556 GTGGCTTTAAGCTCTGCTGATTTTGCAGCCCTTAATGAATAC 3599  
 Db 3789 ATGGTGTTCAGCTCTTGTCTGAATATGAGATTCAGATGCTTAC 3832

RESULT 9  
 US-09-976-594-924  
 Sequence 924, Application US/09976594  
 Patent No. 6673549  
 GENERAL INFORMATION:

APPLICANT: Furness, Michael  
 APPLICANT: Buchbinder, Jenny  
 TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
 FILE REFERENCE: PA-0041 US  
 CURRENT APPLICATION NUMBER: US/09/976,594  
 CURRENT FILING DATE: 2001-10-12  
 PRIOR APPLICATION NUMBER: 60/240,409  
 PRIOR FILING DATE: 2000-10-12  
 NUMBER OF SEQ ID NOS: 1143  
 SOFTWARE: PERL Program  
 SEQ ID NO 924  
 LENGTH: 2802  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: Incyte ID No. 6673549 481118.7  
 NAME/KEY: unsure  
 LOCATION: 1873, 2029  
 OTHER INFORMATION: a, t, c, g, or other  
 US-09-976-594-924

Query Match 1.1%; Score 45.4; DB 4; Length 2802;  
 Best Local Similarity 48.3%; Pred. No. 0.02; 136; Indels 0; Gaps 0;  
 Matches 127; Conservative 0; Mismatches 127; Indels 0; Gaps 0;  
 QY 629 TGAATGACGACATATTATCAATCATTTTCAGGTTTCAGAAATATGTATTACCAAAATTTG 688  
 Db 1272 TAAATGCTGAAGTTACTATAAGAAAGCTTTGGCTTTGGATGAGACTTTTAAAGATGCGAG 1331  
 QY 689 AAGTGACTTTGCACACACCATTTATTTCTTCTATGATTTCTAAGCATTTAAATGGTACCA 748  
 Db 1332 AGGATGCTTTGCAGAAACTTCATAAATATATGAGAAATCTTTGGAAATTAAGAGAAAAC 1391  
 QY 749 TCAGGCAAAAGTATACATATATGGGAAGCAGTGAAGGAGAGACGTAACGCTTACATTTTAC 808  
 Db 1392 AAGCTGAAGGAGAAAGACGACGAAACAAAGAAATAGAAACAGTGCAGAAAAGTTGC 1451  
 QY 809 CTTTATCCTTTTGGGAAAGAGAAATAATTACAAAACATTTACAAAATTAATGATTAATGGATCTG 868  
 Db 1452 GTAACTGCTTAAAGAGAGAGAGAGGCTTAAAGAGAAAGAGAAATCAACTTCTCTT 1511  
 QY 869 CAAACTTCTCTTTTAATGATGAA 891  
 Db 1512 CAACTGTTCTTCTGCTGATGAA 1534

RESULT 10  
 US-09-241-606-5  
 Sequence 5, Application US/09241606  
 Patent No. 6472140  
 GENERAL INFORMATION:  
 APPLICANT: Tanzi, Rudolph E.  
 APPLICANT: Kovacs, Dora  
 APPLICANT: Saunders, Aleister J.  
 TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for  
 FILE REFERENCE: 0609.4460003  
 CURRENT APPLICATION NUMBER: US/09/241,606  
 CURRENT FILING DATE: 1999-02-02  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 333  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(333)  
 OTHER INFORMATION: A Binding Domain  
 US-09-241-606-5

Query Match 1.0%; Score 44; DB 4; Length 333;







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OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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Query Match 1.0%; Score 41.4; DB 4; Length 1664976;
Best Local Similarity 52.0%; Pred.No. 28;
Matches 93; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 3725 TTGTATATATGTAAGGCTTCTGGGTCTTCTAGAGACGAGATCTATCCAAATCAAG 3784
Db 539968 TTGGAGCTACTGATATGCTTACATCTATGCAACAGGAGAAACATGATTAAAGTGCCAA 539909

QY 3785 AAGCTTTGATTAGATGTTGCTCTTAAAGAAATTAAGATGATCTCAATCATGTGATT 3844
Db 539908 AAACAATTAGGCTAGATATAGTTGCAAAAAATGAAATGTTCTGCCAAAGATATTGTTT 539849

QY 3845 TCAATGTGTACAAAGCTTTTCGGGCCCGGCTAGGAGTGGCATGGCTCTTATGGAAGTT 3903
Db 539848 TAAGGTTTGTAAAGAAATTCGGAGAGAGAGGAGCAACATACATGCTATTGATATGTT 539790
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Search completed: August 18, 2004, 00:43:10  
Job time : 288 secs

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